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Result
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Perfect score:
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PYRD_ECOLI
Z238_HUMAN
Z238_MOUSE
Z238_RAT
CU05_HUMAN
TYSY_CRYNE
                                        KKK1_YEAST
PYRD_ECOL6
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SYL_TREPA
RPOC_HAEIN
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UL25_HSV7J
DCTB_RHIME
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CLC1_SCHPO
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61.339 Million cell updates/sec
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P41969
Q50595
P50197
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                                                                                                         7 homo sapien
3 drosophila
9 escherichia
1 macaca fasc
3 drosophila
3 mus musculu
9 anopheles g
6 schizosacch
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methylobact
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42	42	42.5	42.5	42.5	43	43	43	43	43	43	43
29.8	29.8	30.1	30.1	30.1	30.5	30.5	30.5	30.5	30.5	30.5	30.5
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w	Q9i8h3	Q9hsa4	P35811	P05459	P46590	027041	Q02168	Q52963	Q8ze12	Q9hb09	Q8d8g5
rattus norv	xenopus lae	halobacteri	fibrobacter	escherichia	candida alb	methanobact	african hor	rhizobium m	yersinia pe	homo sapien	vibrio vuln

ALIGNMENTS

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RESULT 1
SMAC_HUMAN
     SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

TISSUE=Muscle, and Uterus;

Strausser R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Strausser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.

Diatchenko L., Marusina K., Faramer A.A., Rubin G.M., Hong L.,

Scheet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMAC_HUMAN
Q9NR28; Q96L
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Du C., Fang M., Li Y., Li L., Wang X.; "Smac, a mitochondrial protein that promotes cytochrome caspase activation by eliminating IAP inhibition."; Cell 102:33-42(2000).
                                                                                                                                                                                    Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Nagai K., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; "Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                       Submitted [5]
                                                                                                                                                                                                                                                                                                                                                         "Molecular determinants of the caspase-promoting activity Smac/DIABLO and its role in the death receptor pathway."; J. Biol. Chem. 275:36152-36157(2000).
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2), AND CH
PubMed=10950947;
Srinivasula S.M., Datta P., Fan X.J.,
Alnemri E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1). Watanabe K., Kumagai A., Itakur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Smac protein, mitochondrial precursor (Second mitochondria-derived activator of caspase) (Direct IAP binding protein with low pI).
                                                                                                                                                                                                                                                                                                 TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Soares M.B., Bonaldo M.F., Casavant T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD; P
; Q9BT11; Q9HAV6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION
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A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                              EMBL; AK057778; BAB7155
EMBL; BC004417; AAH0441
PDB; ITEW; 13-SEP-00.
PDB; IG3F; 10-JAN-01.
PDB; IG3F; 10-JAN-01.
PDB; IG73; 10-JAN-01.
                                                                                                                                                                                                                       EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formaticing the statement is not removed. Usage by and formatical statement is not removed.
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[7]
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MEDLINE-20426096; PubMed-10972280;
Chai J., Du C., Wu J.W., Kyin S., Wang
"Structural and biochemical basis of;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu Z., Sun C., Olejniczak E.T
Herrmann J., Wu J.C., Fesik S.
"Structural basis for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:1004-1008(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21020961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 56-64 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smac/DIABLO.
                                                                                                                                                                                                                                                                                        tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                 L; AF262240; AAF87716.1;
L; AK024708; BAB14994.1;
L; AF29870; AAG22077.1;
L; AK057778; BAB71568.1;
L; BC004417; AAH04417.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SPLEEN, PROSTATE AND OVARY. LOW IN BRAIN, LUNG, THY PERIPHERAL BLOOD LEUKOCYTES.

DOMAIN: The mature N-terminus mediates interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIRC7.
SUBCELLULAR LOCATION: MITOCHONDRIAL BUT RELEASED WHEN CELLS UNDERGO APOPTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PROMOTES APOPTOSIS BY ACTIVATING CASPASES IN TOTOCHROME C/APAF-1/CASPASE-9 PATHWAY. ACTS BY OPPOSING INHIBITORY ACTIVITY OF INHIBITOR OF APOPTOSIS PROTEINS (SUBUNIT: Homodimer. Interacts with BIRC2, BIRC3, BIRC4/)
                                                                                                                                                                                                                                                                                                                                                                                                                                 BIRC4/XIAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event-Alternative splicing; Named isoforms-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOId=09NR28-2; Sequence=VSP_004397;
FISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED WITH HIGHEST EXPRESSION
IN TESTIS. EXPRESSION IS ALSO HIGH IN HEART, LIVER, KIDNEY,
SPLEEN, PROSTATE AND OVARY. LOW IN BRAIN, LUNG, THYMUS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9NR28-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406:855-862(2000).
                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synonyms-Diablo-S;
                                          C:mitochondrion; TAS.
P:caspase activation via cytochrome
P:induction of apoptosis via death of
P:induction of apoptosis; TAS.
                                Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11140637;
 55
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                                Apoptosis;
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                            Alternative splicing;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouakenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouakenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C.,
RA Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H.,
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Smac protein, mitochondrial precursor (Second mitochondria-derived
activator of caspase) (Direct IAP binding protein with low pI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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                                                                                                                                             "Functional annotation o Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by binding to and antagonizing IAP Cell 102:43-53(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
SITE
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20383537; PubMed=10929712;
Verhagen A.M., Ekert P.G., Pakusch M.,
Reid G.E., Moritz R.L., Simpson R.J.,
"Identification of DIABLO, a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/c;
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EUNCTION: PROMÓTES ÁPOPTOSIS BY ACTIVATING CASPASES IN THE CYTOCHROME C/APAF-1/CASPASE-9 PATHWAY. ACTS BY OPPOSING THE INHIBITORY ACTIVITY OF INHIBITOR OF APOPTOSIS PROTEINS (IAS SUBUNIT: Homodimer. Interacts with BIRC2, BIRC3, BIRC4/XIA
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                                                                                                                                                                               of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .08;
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/FTId=VSP_004397.
/FTId=VSP_004397.
K -> E (IN REF. 4).
K -> R (IN REF. 2).
MISSING (IN REF. 4).
E -> K (IN REF. 4).
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Pred. No. 3e-14;
Mismatches
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WHKTVTIGFGVTLCAVPIA -> MKSDFYF (in
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; Murinae; Mus
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RESULT 3
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Best Local
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01-NOV-1997
15-SEP-2003
                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., 'Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SITE
CONFLICT
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TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
15-SEP-2003 (Rel. 42,
Hypothetical 64.0 kDa
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                          EMBL; Z46659;
PIR; S49754; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                          Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: HIGHEST EXPRESSION FOUND IN HEART, LIVER, KIDNEY AND TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIRC4/XIAP (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIRC7 (By similarity). SUBCELLULAR LOCATION: MITOCHONDRIAL BUT RELEASED INTO THE CYTOSOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHEN CELLS UNDERGO APOPTOSIS
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1 53 MITOCHONDRION (BY SIMILARITY).
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                             ; CAA86632.1;
S49754.
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96.78;
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Last annotation updat
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W; E53E6F04F1C390Al (
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RESULT 4
YNE2_CAEEL
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J. Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                WormPep; R08D7.2; CE002
Pfam; PF04181; DUF408;
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical R08D7.2.
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01-APR-1993
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TRANSMEM 61 81 POTENTIAL.
                                                                                                        SEQUENCE
                                                                                                                                                                        EMBL; Z12017; CAA78048.1;
                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                        elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993
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                                                                                                                     Hypothetical protein
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PIAEKSEP--VDSQFKKEPSIWLVTDS 165
                         PIAQKSEPHSLSSEALMRRAVSLVTDS
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                                                                                                       455 AA;
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41:7%;
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Caenorhabditis.
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RESULT 5
ELK1_MOUSE
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                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                Phosphorylation.
DNA_BIND 5
                                                                                                                                                                                                                                                                                           Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0454; ETSDOMAIN. SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T05013; -. MGD; MGI:101833; Elk1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JC4965; JC4965.
HSSP; P28324; 1BC8.
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-!- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grevin D., Ung S., Denhez F., Denem Stehelin D., Martin P.; "Structure and organization of the Gene 174:185-188(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6; TISSUE=Embryo;
MEDLINE=97017146; PubMed=8863747;
Grevin D., Ung S., Denhez F., Deh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ETS-domain protein ELK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00178; Ets;
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01-NOV-1995
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MEDLINE=95047310; PubMed=7958835;
Medra S.-M.,
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InterPro; IPR002341; HSF_ETS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN
LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
SIMILARITY: BELONGS TO THE ETS FAMILY.
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10; Conser
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PS00346;
PS50061;
                                      AQKSEPHSLSSEALMRRAVSLVTDST
AVKAEPEVSASEGLLARLPAILTENT
                                                                                                                                                                                               429 AA;
                                                                                                                                                                                                                              133
                                                                                              Conservative
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ETS_DOMAIN_2; 1.
ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                         86
133
                                                                                                                                                                                                  45243 MW;
                                                                                                                        35.5%;
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P -> T (IN REF
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                         protein;
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ed by Ras.";
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RESULT 6
YI38_MYCTU

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SMART; SM00670; PINC; 1.
Hypothetical protein; Complete
SEQUENCE 131 AA; 14726 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98295987; pubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy, Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YI38_MYCTU STANDARD; PRT; 131 AA. 050595; P95168; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein Rv1838c. OR MTCY359.35.
                                                                                                                                                                                                                                                                                                                                                  TubercuList; Rv1838c; ...
InterPro; IPR002716; PIN.
InterPro; IPR006596; PINc.
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z83859; CAB06116.1; -. EMBL; AE007047; AAK46157.1; PIR; E70663; F70663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg (
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula )
                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; MT1886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinon
Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1773;
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                                                                                                                                                                                                                              Similarity
                                                                                                                                         SHPHKLDAQRLLESALSGGERLVTDA 41
                                                                                                                                                                        SEPHSLSSEALMRRAVS----LVTDS 29
                                                                                                                                                                                                              Conservative
                                                    STANDARD;
                                                                                                                                                                                                                            33.3%;
Created)
 sequence update)
                                                                                                                                                                                                              5.
                                                                                                                                                                                                                              Score 47; I
Pred. No. 3
                                                    PRT;
                                                                                                                                                                                                                                                                             proteome.
C164346E951BFE7E CRC64;
                                                                                                                                                                                                              Mismatches
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8
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                                                                                                                                                                                                                                              Length 131;
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RAC OCC MACOOK M
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28-FEB-2003
15-SEP-2003
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
"Cloning and sequencing of a 2.5-dichloro-2,5-cyclohexadiene-1,4-diol
dehydrogenase gene involved in the degradation of gamma-
hexachlorocyclohexane in Pseudomonas paucimobilis.";
J. Bacteriol. 176:3117-3125(1994).
-!- PUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
(2,5-DDCL) INTO 2,5-DICHLOROHINONE (2,5-DCHQ).
-!- PATHWAY: Gamma-hexachlorocyclohexane degradation; third step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D14595; BAA03444.1; -. HSSP; P19992; 1HDC: InterPro; IPR002198; ADH_short. Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was use, by non-profit institutions as long as its content is in no was
                           STRAIN-C57BL/6J; TISSUE-Mammary gland;
MEDLINE-22388257; PubMed-12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TBC1 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CV04_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94252977; PubMed-7515041; Nagata Y., Ohtomo R., Miyauchi K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sphingomonadaceae; NCBI_TaxID=13689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas paucimobilis (Sphingomonas paucimobilis).
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (2,5-DDOL dehydrogenase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (Rel. 41, Created)
3 (Rel. 41, Last sequence of the sequence
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250 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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25644 MW;
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Rodentia;
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   K., Farmer A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
annotation update)
C22orf4 homolog (Fragment).
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Pred. No.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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   Rubin G.M.,
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                  Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YMH6_YEAST STANDARD; PRT; 944 AA. Q03631; Q1-NOV-1997 (Rel. 35, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Putative 107.6 kDa transcriptional regulatory
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InterPro; IPR001195; RabGAP_TBC.
Pfam; PF00556; TBC; 1.
SMART; SM00164; TBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  STRAIN-S288c / PubMed-9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi;
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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                                                                               -!- SUBCELLULAR
                                                                                                                                      Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intergenic region.
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                                                    domain.
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                / AB972;
                                                                                  Contains
                                                                               LOCATION: Nuclear (Probable).
Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetaceae;
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39.1%;
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B16BD293761D4A53 CRC64;
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Abramson R.D., Mullahy S.J.,
Malek J.A., Gunaratne P.H.,
a A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Casavant T.L.,
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Cal S., Arron-
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"Identification, characterization, and intracellular processing
ADAM-TS12, a novel human disintegrin with a complex structural
organization involving multiple thrombospondin-1 repeats.";
J. Biol. Chem. 276:17932-17940(2001).
-i- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Secreted. Associated with the extracel
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P58397;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADAMTS-12 precursor (EC 3.4.24.-) (A disintegrin and metality matching the distribution of the distri
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PROSITE; PS50048; ZN2_CY6_FUNGAL_2; FALSE_NEG.

Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Metal-binding.

DNA_BIND 76 109 ZN(2)-CYS(6), FUNGAL-TYPE.
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InterPro; IPR001138; Fungi_TrN.
SMART; SM00066; GAL4; 1.
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                                                                                                                                                                                    PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.
PTM: IS SUBJECTED TO AN INVRACULULLAR MATURATION PROCESS
TO A FRACMENT CONTAINING THE N-TERMINAL REGION INCLUDING
METALLOPROTEINASE, DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DO
                                                                                                                                                                                                                                                                         DOMÀIN: THE SPACER DOMAIN AND FOR A TIGHT INTERACTION WITH 7 SIMILARITY).
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TISSUE SPECIFICITY: Exp
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                                                                                                                                                                   C-TERMINAL FRAGMENT
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PF00090; tsp_1; 6.
PF00090; TSP1; 8.
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IPR002870; Pep_M12B_propep.
IPR001590; Reprolysin.
IPR000884; TSP1.
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                                                              ΑĄ,
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                                                                                                                                                                                                                                                                                                                                                                                                         CYSTEINE_SWITCH; FALSE_NEG DISINTEGRIN_1; FALSE_NEG. DISINTEGRIN_2; FALSE_NEG.
                                                                     1503
                                                                                                                                                                                                                                                                                                                           240
1593
464
544
597
                                                                             402
125
215
2485
685
790
951
1104
1275
1300
1320
1371
                                                                                                                                                                                                                                                                                                                                                                                          ZINC_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                  TSP1;
                                                                                                                                                                                                                           826
882
942
996
1315
1365
1365
1421
1421
1470
1531
1531
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADAM_MEPRO;
                                      32.3%;
                                                              177545
               EPHSLSSEALMRRAVS
                                                                                                                                                                                                                                                                                                                                                                                 Zinc;
                                                             N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
MW; 07F9F48E63BD83A3
                                                                                                                                                                                    CYSTEINE SWITCH ()
ZINC (CATALYTIC)
BY SIMILARITY.
ZINC (CATALYTIC)
ZINC (CATALYTIC)
                                                                                            N-LINKED
N-LINKED
                               Score
Pred.
6; Mis
                                                                                                                    N-LINKED
                                                                                                                                    N-LINKED
                                                                                                                                                    N-LINKED
                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                           TSP TYPE-
TSP TYPE-
TSP TYPE-
TSP TYPE-
POLY-GLU.
PLAC.
                                                                                                                                                                                                                                                                                                                   TSP TYPE-
CYS-RICH.
                                                                                                                                                                                                                                                                                                   SPACER
TSP TYF
                                                                                                                                                                                                                                                                            SPACER
                                                                                                                                                                                                                                                                                   TSP
                                                                                                                                                                                                                                                                                                                           TSP TYPE-1 1.
                                                                                                                                                                                                                                                                                                                                                          POTENTIAL BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                          METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                    ADAMTS-12
                                                                                                                                                                                                                                           TYPE-1
TYPE-1
TYPE-1
TYPE-1
                                                                                                                                                                                                                                                                                  TYPE-1
                                                                                            CATALYTIC) (
ENKED (GLCNAC.
NKED (GLCNAC.
                               smatches
                                                                                                                                                                                                                                                                                                                                                                                 Signal; Glycoprotein; Zymogen;
                                      45.5;
No. 1
                                                                                                                                                                                                                                            8765
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                              .2e+02;
.es 6;
243
               24
                                             DВ
                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                    (BY
(BY
                                                                                                                                                                                                            (BY
                                             Length 1593;
                                                                                                                                                                                            SIMILARITY).
                                                                                                                                                                                                            SIMILARITY)
                               Indels
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(POTENTIAL).
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                               Gaps
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Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Mamantides P.G., Scherer S.E., Li P.W. Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Bellew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Bellew R.M., Basu A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gersen K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bellew R.M., Bulley S., Danke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gersen K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Godek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Godek A., Gong F., Gorrell J.H., Gu Z., Kennison J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Moylan R., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., McDarry C., Morris J., McPherson D.L.,
RA Merkulov G., Milshina N.V., McDarry C., Morris J., Noshrefi A.,
RA Merkulov G., Milshina N.V., McDarry C., Murphy L.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., McDarry G., Nucheta J.R., Purit V., Reese M.G.,
RA Harris N.L., Bayr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
VAF2_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VNL3;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable vacuolar ATP synthase subunit F 2 (EC 3.6.3.14) (V-ATPase F subunit 2) (Vacuolar proton pump F subunit 2) (V-ATPase 14 kDa subunit 2)
                        This SWISS-PROT entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG1076.
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                                                peripheral catalytic v
an integral membrane v
c' and d) (By similar
SIMILARITY: Belongs to
                                                                                                                                         H(+)(Out).
SUBUNIT: V-ATPase
                                                                                                     integral membrane v0
  ROT entry is copyright. It is produ
Swiss Institute of Bioinformatics
                                                        (By similarity). Belongs to the V-ATPase F subunit family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                         v1
                                                                                                 proton
                                                                                                                       complex (components
                                                                                                                                           heteromultimeric
                                                                                                 pore
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RESULT 12

NRFD_ECOLI

ID NRFD_ECOLI

AC p32709;

DT 01-CCT-1993

DT 01-CCT-1993

DT 01-CCT-2001

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OC Enterobactes

OX NRFD OR BACTORICA

RA HUSSAIN H.A.

RT "A Seven-ger

RT reduction tr

RA HUSSAIN H.A.

RT "A SEVEN-GER

RY MEDLINE=940;

RN [2]

RP SEQUENCE FR

SEQUENCE FR

SEQUENCE FR

CO TRAIN=S12,

RA HUSSAIN H.A.

RT "ANALYSIS OI

RA BLATTNEF 940;

RA BLATTNEF 940;

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RY "ANALYSIS OI

RY
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P32709;
01-OCT-1993
01-OCT-1993
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0037402; CG1076.
InterPro; IPR005772; ATPSynt_Feuk.
InterPro; IPR002641; ATPSynt_Fsub.
Pfam; PF01990; ATP-synt_F; 1.
ProDom; PD003811; ATPSynt_F; 1.
TIGRPAMS; TIGR01101; V_ATP_synt_F; 1.
Hydrolase; ATP synthesis; Hydrogen ion transport.
SEQUENCE 124 AA; 14132 MW; 0C5093AFDF0006BAB C
                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 21:5408-5417(1993).
-- FUNCTION: PROBABLY INVOLVED IN THE TRANSFER OUTNOME POOL TO THE TYPE-C CYTOCHROMES.
-- SUBCELLULAR LOCATION: Integral membrane protections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A seven-gene operon essential for formate-dependent nitrite reduction to ammonia by enteric bacteria.";
Mol. Microbiol. 12:153-163(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=94335626; PubMed=8057835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NrfD protein.
NRFD OR B4073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of the Escherichia coli genome. region from 89.2 to 92.8 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Daniels D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blattner F.R., Burland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94089392; PubMed=8265357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003600; AAF51917.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                   X72298; CAA51044.1;
U00006; AAC43167.1;
AE000480; AAC77043.
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                      TO W. SUCCINOGENES POLYSULFIDE REDUCTASE CHAIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27, Created)27, Last sequence update)40, Last annotation updat
                                                                                                                                                                                                                            institutions as long as
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32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V.D., Plunkett G.
                                                                                                                                                                                                                                                                                                                                                                                                     Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45;
Pred. No. 7
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                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                            its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence of
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PIR; H65215; D57987

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RESULT 13
CV04_MACFA
ID CV04_M
AC 095KI1
DT 28-FEB
DT 28-FEB
DT 28-FEB
DT 28-FEB
DT 28-FEB
CC GECOP
OX MACACA
OC CACCOP
OX MACACA
CC CACCOP
OX NCBI_T
RN [1]
RP SEQUEN
RC TISSUE
RA OSAGA
RT Librar
RI Librar
RI Librar
RI Librar
RI Submit
CC -----
CC This S
CC betwee
CC the Eu
CC the Eu
CC crep
CC the Eu
CC sentiti
CC entiti
CC entiti
CC entiti
CC entiti
CC sentiti
CC SMART;
DR SMART;
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DR SMART;
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Best Local
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
7RC1 domain family protein C22orf4 homolog (Q
                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                           SEQUENCE
                                                                                                                                  NON_TER
                                                                                                                                               PROSITE; PS50086; TBC_RABGAP; 1.
                                                                                                                                                              Pfam; PF00566; TBC; : SMART; SM00164; TBC;
                                                                                                                                                                                                                                                                                                                            libraries.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 Rab-GAP TBC domain.
                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Temporal cortex;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
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TRANSMEM
                                                                                                                                                                        INBL; ABUUUUU
InterPro; IPR000195; R
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                    EMBL; AB060857; BAB46876.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Macaca.
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TRANSMEM 1
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sen the Swiss Institute of Bioinformatics and the Ev
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                                                                  Similarity
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9; Conser
AVTLGGTSDPGTLSSSALSEREAS 176
                         AVPIAQKSEPHSLSSEALMRRAVS
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497 AA;
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Primates;
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                                                  Score 45; DB Pred. No. 37; 3; Mismatches
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                                                                                                    RAB-GAP TBC.
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-> A (IN REF. 2).
BC5B3EF031D5CE29 CRC64;
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                                                                           DB 1; Length 497;
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                                                   Indels
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TUD_DROME
                                                                                              Matches
                                                                                                                     Query Match
Best Local
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DOMAIN
                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0003891; tud.
G0; G0:0019090; P:mitochondrial rRNA, mitochondrial export;
G0; G0:0007315; P:pole plasm assembly; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION OF PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
-!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
-!- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR REGION OF THE DEVELOPING OOCYTE DURING THE EARLY TO MIDDLE STAGES
                                                                                                                                                                                                                   DOMAIN
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PROSITE; PS50304; TUDOR; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00567; TUDOR; 10 SMART; SM00333; TUDOR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X62420; CAA44286.1; PIR; A41519; A41519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Golumbeski G.S., Bardsley A., Tax F., Boswell R.E., "Tudor, a posterior-group gene of Drosophila melanogaster, novel protein and an mRNA localized during mid-oogenesis.", Genes Dev. 5:2060-2070(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUD
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01-MAY-1992 (Rel. 22,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001097; Maternal_tudor InterPro; IPR002999; Tudor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 9 Tudor domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
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8; Conser
                                          VPIAQKSEPHSLSSEALMRRAVSLVT 27
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                                                                                              Conservative
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RESULT 15
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R InterPro; IPR006134; DNA_pol_B_dom.
R InterPro; IPR006134; DNA_pol_B_exo.
R InterPro; IPR006133; DNA_pol_B_exo.
R InterPro; IPR006133; DNA_pol_B_exo.
R InterPro; IPR006133; DNA_pol_B_exo.
R Pfam; PF003104; DNA_pol_B; 1.

DR Pfam; PF003104; DNA_pol_B_exo; 1.

DR PRINTS; PR00106; DNA_pol_B_exo; 1.

DR RINTS; SM00486; POLBC; 1.

DR TIGRFAMS; TIGR00592; pol2; 1.

DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.

DR TRANS; PS00116; DNA_POLYMERASE_B; 1.

DR TRANS; DNA_repair; Nuclear protein; Zinc-finger.

KW Transferase; DNA_repair; Nuclear protein; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                            CONFLICT
CONFLICT
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Biochem. Biophys. Res. Commun. 219:795-799(1996).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutat.
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q61493; Q9JMD6; Q9QWX6;
30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (Seizure related protein 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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     CONFLICT
                                                                                                                                                                                   ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugaya E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kajiwara K., Nagawawa H., Shimizu-Nishikawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain neurons."
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STRAIN-129/Ola; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kajiwara
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                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1337131; Rev31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular characterization of seizure-related genes isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   + {DNA}(N)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB031049;
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C4-TYPE
C4-TYPE
G -> N
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                                                                                                    -> A (IN REF. 2).
-> T (IN REF. 2).
-> Q (IN REF. 2).
                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ookura T.,
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                                  Matches
                                         Query Match
Best Local
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CONFLICT
SEQUENCE
1226 AIPADEKMKPHSEAELTPNHQSVSELTSSS 1255
           1 AVPIAOKSEPHSLSSEALMRRAVSLVTDST 30
                                  l Similarity
10; Conserv
                                                                   1848
2368
3122
                                  Conservative
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2368
                                         31.9%;
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                                                                  A ->
V ->
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                                         Score 45; I
Pred. No. 3.
                                  Mismatches
                                                                  > T (IN REF. 2).
> G (IN REF. 3).
A39846CAF7365BA8 CRC64;
                                                   DB 1;
                                           .2e+02
                                  12;
                                                 Length 3122;
                                  Indels
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Search completed: October Job time : 24 secs

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2003, 09:37:22

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Result
No.
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being primard is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   October 2, 2003, 09:35:22; Search time 77 Seconds (without alignments) 61.842 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //SIDS1/gcgdata/geneseq/geneseqp-emb1/Aa1989_DAT:*
//SIDS1/gcgdata/geneseq/geneseqp-emb1/Aa1990_DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA191.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*
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AAU78435
AAU78436
AAU78436
AAU78430
ABG72302
AAB54139
AAB54139
AAB56210
AAU78447
ABP72164
                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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                     Inhibitor of apopt
Human partial sequ
Human pancreatic c
Human caspase acti
Inhibitor of apopt
                                                                                                                                                                                                                                                                                              Description
Human DIABLO/Smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   being printed,
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4 5	44	43	42	41	40	39	38	37	36	<u>ა</u>	34	ω ω	32	31	30	29 .	28	27	26	25	24	23	22	21	20	19	18	17	16	5	14	13	12	11	10
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2161	2038	1018	809	809	809	809	809	644	355	173	124	44	182	594	499	384	352	336	312	312	284	272	2045	944	710	396	73		13	15	20	186	84	237	239
22	23	22	23	23	23	23	23	22	23	22	22	22	22	22	21	21	23	22	24	22	23	22	22	23	23	22	24	24	24	24	23	22	24	24	24
аам78959	AAE25098	ABB62522	AAE15986	AAE15985	AAE15984	AAE15983	AAE15982	ABG05466	ABP66105	AAU48666	ABB57798	ABB12208	ABU53172	ABB61195	AAG41345	AAG54380	ABP29265	AAU27891	ABP55411	AAU27719	ABG79600	AAG66438	ABB61941	ABP35704	ABP69647	AAU51015	ABG72304	ABG72316	ABG72314	ABP71314	ABB76208	AAB92922	ABG72303	ABG72301	ABB82743
Human protein SEQ	Human kinase and p	3				-	Human cyclic nucle	Novel human diagno	Bifidobacterium lo	Propionibacterium	Drosophila melanog	Human secreted pro	Human testes-deriv	Drosophila melanog	Arabidopsis thalia	Arabidopsis thalia	Streptococcus poly	Human contig polyp		Human full-length	Vernonia ribonucle	Human ATPase 30.		Fungal ZBC protein	Human polypeptide	Propionibacterium	Ω.	Human pro-apoptoti	Human pro-apoptoti		Human smac (DIABLO	Human protein sequ	Rat partial sequen	pro-a	Human Smac polypep

ALIGNMENTS

RESULT 1 AAU78435

AAU78435 standard; Peptide; 30

AAU78435;

18-JUN-2002 (first entry)

Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N30

Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2; Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy; neoplastic cell; mutant; tumour.

Homo sapiens

Synthetic.

WO200216418-A2

28-FEB-2002.

24-AUG-2001; 2001WO-US26492

24-AUĢ-2000; 2000US-227735P.

(UYJE-) UNIV JEFFERSON THOMAS

Alnemri

WPI; 2002-304115/34

Novel Smac peptides and polynucleotides encoding the peptides, useful

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RESULT 2
AAU78439
ID AAU7
XX
AC AAU7
XX
IDT 18-J
XX
Inhi
XX
INH
DE Inhi
XX
Huma
KW Huma
KW Heop
XX
INH
OS
Homo
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WO20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC (a) separately contacting several cell populations expressing a cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (BC12 interacting CC (b) incubating the cell populations with a direct stimulus of the cell domain) with a compound to be tested for apoptotic inhibiting activity; (b) incubating the cell populations with a direct stimulus of the cell death pathway; and (c) measuring the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity is indicative that the compound is an inhibitor of apoptosis. (I) and (II) CC are useful for inducing apoptosis in a cell. The Smac polypeptide and cell polynucleotide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase-7 or CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-7 or CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-CC mediated apoptosis which involves contacting a cell transformed or CC call viability indicates the presence of an inhibitor and decrease in CC cell viability indicates the presence of an enhancer. Optionally, the cell viability indicates the presence of an enhancer optionally, the cell viability indicates the presence of large and small caspase coll viability indicates the presence of large and small caspase in the presence of an enhancer. Optionally, the cell viability indicates the presence of large and small caspase to cell viability indicates the presence of large and small caspase the presence of an enhancer. Preferably, the large and small subunits of caspase-7 or caspase-7 or caspase-9 are detected. (I) is also useful for cidentifying a compound that inhibits smac binding to Smac-binding correspondence of an 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 30
24-AUG-2001; 2001WO-US26492
                                                                                                                                Homo
                                              28-FEB-2002
                                                                                    WO200216418-A2
                                                                                                                                                                           neoplastic cell;
                                                                                                                                                                                                                                                    Inhibitor of apoptosis (IAP) protein Smac, peptide Smac-N35.
                                                                                                                                                                                                                                                                                                     18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                  AAU78439;
                                                                                                                                                                                                                                                                                                                                                                                       AAU78439 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated Smac peptide or polypeptide (I) and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 7; 78pp; English
                                                                                                                                sapiens
                                                                                                                                                                                             interacting
                                                                                                                                                                      inhibitor of apoptosis; IAP; Smac; nteracting domain; caspase; BIR domastic cell; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVPIAQKSEPHSLSSEALMRRAVSLYTDST 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compounds
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Pred. No. 2.2e-16;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                        mac; apoptosis; BID; BIR1; BIR2;
domain; BIR3; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 3 AAU78436

AAU78436 standard; Peptide;

В δÃ

1 AVPIAQKSEPHSLSSEALMRRAVSLVTDST 1 AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30

30

Matches Query Match Best Local

30;

Conservative

0;

Local Similarity

100.0%;

Length Indels

0;

0

X X E X E X X X

18-JUN-2002 AAU78436;

(first entry)

Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2;

Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N39

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The invention relates to an isolated Smac peptide or polypeptide (I) CC and an isolated nucleic acid (II) encoding (I). Also described is a CC method of identifying a compound that inhibits apoptosis, comprising: CC (a) separately contacting several cell populations expressing a CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (BCl2 interacting CC domain) with a compound to be tested for apoptotic inhibiting activity; (C) includating the cell populations with a direct stimulus of the cell (CC (b) includating the cell populations with a direct stimulus of the cell cell pathway; and (c) measuring the specific apoptotic activity is condicative that the compound is an inhibitor of apoptosis. (I) and (II) CC are useful for inducing apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase-7 or CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-CC mediated apoptosis which involves contacting a cell transformed or transforted with a vector expression (I) with a centilete inhibitor.
                                                                                                                                                                                                                                         transfected with a vector expressing (I) with a candidate inhibitor or candidate enhancer; and detecting cell viability, where an increase in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an enhancer. Optionally, the method involves detecting the presence of large and small caspase subunits after contacting cell transformed with the vector expressing (I), with the candidate compound. A decrease in processing indicates the presence of an enhancer. Preferably, the large and small subunits of caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for identifying a compound that inhibits Smac binding to Smac-binding or BID3.
                                                                                                                                                                      identifying a compound that inhibits Smac binding to Smac-binding molecule (a portion of IAP e.g. a BIR domain such as BIR1, BIR2 or BIF or a full-length IAP). (II) is useful in gene therapy techniques. The present sequence represents the amino acid sequence of Smac peptide
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 47; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       overexpresses inhibitor of caspase, and modulating compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-2000;
                                                                                                       35
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                                                                                                       AA;
Score 141; DB 23;
Pred. No. 2.7e-16;
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CC (a) separately contexting several cell populations expressing a CC cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC cytosolic Smac (a) and an inhibitor of BID (Bcl2 interacting activity; CC and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting activity; CC (b) incubating the cell populations with a direct stimulus of the cell cell pathway; and (c) measuring the specific apoptotic activity of the CC indicative that the compound is an inhibitor of apoptosis. (I) and (II) CC are useful for inducing apoptosis in a cell. The Smac polypeptide and CC polynucleotide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase-3, caspase-7 or CC caspase-9, Preferably, the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-CC mediated apoptosis which involves contacting cell transformed or transfected with a vector expressing (I) with a candidate inhibitor or candidate inhibitor or candidate inhibitor or call viability indicates the presence of an enhancer. Optionally, the cell viability indicates the presence of an enhancer optionally, the cell viability activates the presence of an enhancer. Optionally, the contacting cell transformed with the vector expressing cell transformed with the vector expressing cell caspase in cell viability and an inhibitor and an increase in the processing indicates the presence of an enhancer. Preferably, the large and small caspase the compound that inhibits Smac binding to Smac Phinding contacting cell transformed with the vector expressing indicates the presence of an enhancer. Preferably, the large and small caspase of cell viability and call transformed with the processing indicates the presence of an enhancer. Preferably the large 
                                                                                                                                                                  Query Match
Best Local S
Matches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-2000; 2000US-227735P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bcl2 interacting
neoplastic cell;
                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30
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                                                                                                                                                                                                                                                                                                                                     39
                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        \ensuremath{\mathsf{IAP}}\xspace (II) is useful in gene therapy techniques. The represents the amino acid sequence of Smac mutant
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                                                                                                                                                              Score 141; DB 23;
Pred. No. 3.1e-16;
); Mismatches . 0;
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                                                                                                                                                                                                                                                Length
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Sequence

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RESULT 4
AAU78430
The invention relates to an isolated Smac peptide or polypeptide (I) cand an isolated nucleic acid (II) encoding (I). Also described is a comethod of identifying a compound that inhibits apoptosis, comprising: CC (a) separately contacting several cell populations expressing a cytosolic Smac (a Smac isoform that begins with MKSDPYF sequence, CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (BCl2 interacting CC domain) with a compound to be tested for apoptotic inhibiting activity of the cell populations, where inhibition of the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity is CC indicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac polypeptide and CC polypucleotide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase, where the CC inhibitor inhibits activation or activity of caspase-3, caspase-7 or CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP. CC ill is useful for identifying an inhibitor or enhancer of a caspase-CC mediated apoptosis which involves contacting a cell transformed or call viability indicates the presence of an inhibitor and a decrease in CC cell viability indicates the presence of an inhibitor and a decrease in CC cell viability indicates the presence of an inhibitor and a decrease in CC cli viability indicates the presence of an inhibitor and a decrease in the processing indicates the presence of an inhibitor and small caspase in cell viability indicates the presence of an inhibitor and small subunits of CC aspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for identifying a compound that inhibits Smac binding to Smac-binding conditions of IAP e.g. a BIR domain such as BIR1, BIR2 or BIR3, CC present sequence represents the N-terminal amino acid sequence of Smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis modulating compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU78430 standard; Peptide; 40 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-304115/34
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Bcl2 interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibitor of apoptosis (IAP) protein Smac, N-terminal peptide
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RESULT 5
ABG72302
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        binding molecule that specifically binds to DIABLO or its fragment, detecting DIABLO in a biological sample (by contacting the sample with an IAP and detecting the presence of an IAP/DIABLO complex), modulating the death of a cell (by contacting a cell with an agent, which modulates the level and/or functional activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO relate condition comprising an agent which reduces the level/activity of a polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is useful for screening for an agent which modulates cell death. An antigen binding molecule is useful for detecting DIABLO in a biological
                                                                                                                                                 The invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino aci in length. Also included are the polypucleotide encoding DIABLO, expression vectors, transformed host cells, producing a biologically active fragment of DIABLO (by contacting an inhibitor of apoptosis (1 with a fragment of the polypeptide, and detecting a reduction in acti of the IAP), producing a natural or synthetic variant of DIABLO with cell death activity or which reduces IAP activity, an antigential or synthetic variant of the polypeptide in the polypeptide in the polypeptide in activity or which reduces IAP activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease; neurodegenerative disease; hepatic muscular tissue damage; heart attack; hepatic tissue damage; liver disease; immunogen.
                                                                                                                                                                                                                                                                                      Disclosure; Fig
                                                                                                                                                                                                                                                                                                             death or apoptosis e.g. cancer
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                                                                                                                                                                                                                                                                                                                           pro-apoptotic polypeptide, useful
ulate cell death and for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
  which modulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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Pred. No. 3.2e-16;
Mismatches 0;
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                                                                                                                                                                                                                                          8 amino acids
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                                                                                                                                                                                    in activity
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of
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Best Local
            neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be u in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used
                                                                                                                AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic,
                                                                                                                                                                                Claim 11; Page 1027–1028; 1379pp; English
                                                                                                                                                                                                                            New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a polypeptide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with expression or activation of DIABLO, such as cancer, vascular disease, hepatic disease, autoimmune disease and neurodegenerative disease, tissue damage or muscular tissue damage associated with heart attack, or hepatic tissue damage associated with a liver disease. DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence
                                                                                                                                                                                                                                                                           N-PSDB; AAC98904
                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; diagnosis; identification; cytostatic; neuro, nootropic; immunomodulatory; relaxant; contraceptive; gantiinflammatory; cardiant; gene therapy; chromosome mallinkage analysis; tissue identification; tissue typing;
                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neural;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human pancreatic cancer antigen protein sequence SEQ ID
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                                                                                                                                                                                                                in
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome mapping;
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15;
                                                                                                                                                                                                             particular pancreatic pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202;
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Best Local
                                                                            The present sequence is the human Smac protein. Its coding sequence was isolated by purifying the protein and searching a HeLa cell cDNA library for sequences which bound to probes based upon it. Smac is a mitochondrial protein which is released into the cytosol during apoptosis, and acts as a caspase-3 activator. The protein and its coding sequence can be used to modulate the expression and function of caspases and their activators, and also can be used as drug targets and regulators to promote or inhibit apoptosis in the treatment of cancer and autoimmune and neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular,
                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                              Novel caspase regulatory polypeptides useful for screening binding agents specific for the polypeptides which are useful for diagnosis and also for treating apoptosis associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6110691-A
                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JAN-2000; 2000US-0479309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human caspase activator Smac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB26210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                               Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JAN-2000; 2000US-0479309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agonists and antagonists to the antigens can be screened
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caspase activator; Smac; apoptosis; cancer; autoimmune disease;
egenerative disease; mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                              column 23-24; 16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVPIAQKSEPHSLSSEALMRRAVSLVTDST 73
                                                   239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 AA;
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141; DB 21;
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The invention relates to an isolated Smac peptide or polypeptide (I) cand an isolated nucleic acid (II) encoding (I). Also described is a commethod of identifying a compound that inhibits apoptosis, comprising: CC (a) separately contacting several cell populations expressing a CC cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (BC12 interacting cC domain) with a compound to be tested for apoptotic inhibiting activity; (b) incubating the cell populations with a direct stimulus of the cell ceath pathway; and (c) measuring the specific apoptotic activity of the CC indicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac polypeptide and CC polynuclectide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase-3, caspase-7 or CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-CC mediated apoptosis which involves contacting a cell transformed or transfected with a vector expressing (I) with a candidate inhibitor or call viability indicates the presence of an inhibitor and a decrease in CC cell viability indicates the presence of an inhibitor apparesing cC (I), with the candidate compound. A decrease in processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an anhancer. Preferably, the large and small caspase contacting a cell transformed contacting an inhibitor and an increase in processing indicates the presence of an enhancer. Preferably, the large and small subunits of the presence of an inhibitor and an increase in the processing indicates the presence of an enhancer. Preferably, the large and small subunits of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis modulating compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-304115/34
N-PSDB; ABK15451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 36; Page 73-74; 78pp; English
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neoplastic cell;
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domain; BIR3; gene therapy;
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                                                                                                                                                 The present sequence is the protein sequence for human DIABLO/Smac, an inhibitor of inhibitor-of-apoptosis (IAP) proteins. The invention provides a nucleic acid, such as an antisense coliquoucleotide, which specifically hybridises to a nucleic acid encoding a protein that induces cell death, especially APAFI, RAIDD or Diablo/SMAC. A claimed method for inhibiting a cell's death cell with the nucleic acid under conditions permitting the nucleic acid under conditions permitting the nucleic acid under conditions permitting the nucleic acid to enter the cell, especially the use of a vector, liposome, or a mechanical or electrical means. The method is used to a treat a neurodegenerative disorder, especially a brain disorder or central nervous system disorder, or a heart disorder, especially cardiomyopathy, in a human (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      γ
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                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 23A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Troy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; DIABLO/Smac; cell death; apoptosis;
neurodegenerative disease; heart disease; cardiomyopathy; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DIABLO/Smac
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DB; ABZ58109.
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                                      Similarity
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                                                                                                                   239
             Conservative
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                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding an inhibitor-of-apoptosis protein, useful neurodegenerative disorder or cardiomyopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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100.0%; Pr
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  Score 141; DB 24;
Pred. No. 3.3e-15;
Mismatches 0;
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Pred. No. 3.3e-15;
Mismatches 0;
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RESULT 10
ABB82743
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                                                                                                                                                                                                                                                                                                      cancer patient. The method involves (a) measuring a level of a tumour up-
cregulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic
cell-containing sample from the cancer patient; and (b) comparing the
level of TUCAN in the sample to a reference level of TUCAN, where a low
level of TUCAN in the sample correlates with increased survival of the
patient. Alternatively, the method involves measuring levels of TUCAN and
one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or
Smac in a neoplastic cell-containing sample from the cancer patient. The
method is useful for determining if the patient is at risk for relapse,
or for determining a proper course of treatment for a patient with
cancer. The method is also useful for monitoring the effectiveness of a
course of treatment for a patient with cancer, e.g. colon cancer,
leukemia, CNS cancer, breast cancer, ovarian cancer, lung cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Дb
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining a prognosis for survival for a cancer patient, useful for determining if the patient is at risk for relapse, comprises measuring a level of TUCAN in a sample from the patient, and comparing it to a reference level
                                                                                                                                                                                                                                                                                      present sequence represents a human Smac polypeptide.
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N-PSDB; ABV75367.
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12-FEB-2002;
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AVPIAQKSEPHSLSSEALMRRAVSLVTDST
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2002US-356934P
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                                                                                                                                            Score 141;
Pred. No. 3
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RESULT 11 ABG72301

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Mouse; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepatic autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
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97..10
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73..80
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65..72
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17..24
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  rne invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino acids in length. Also included are the polynucleotide encoding DIABLO, expression vectors, transformed host cells, producing a biologically active fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP) with a fragment of the polypeptide, and detecting a reduction in activity of the IAP), producing a natural or synthetic variant of DIABLO with cell death activity or which reduces IAP activity, an antigenbinding molecule that specifically binds to DIABLO or its fragment, detecting DIABLO in a biological sample (by contacting the sample with an IAP and detecting the presence of an IAP/DIARIO commits.)
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The invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino acids in length. Also included are the polypucleotide encoding DIABLO, expression vectors, transformed host cells, producing a biologically active fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP) with a fragment of the polypeptide, and detecting a reduction in activity of the IAP), producing a natural or synthetic variant of DIABLO
                                                                                                                                                                                                                                                                                   Disclosure; Page 35; 50pp; English
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                             Ota
                                                                                                and/or diagnosis of the full-length cDNAs -
                                                                                                                                                                      Primer sets for synthesizing full-length cDNAs defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a polypeptide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with expression or activation of DIABLO, such as cancer, vascular disease, hepatic disease, autoimmune disease and neurodegenerative disease, tissue damage or muscular tissue damage associated with heart attack to the property of the property o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agent, which modulates the level and/or functional activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO relational condition comprising an agent which reduces the level/activity of a polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is useful for screening for an agent which modulates cell death. An antigen-binding molecule is useful for detecting DIABLO in a biological sample. The agent which modulates the level and/or functional activity of a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB92922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB92922 standard; Protein; 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding molecule that specifically binds to DIABLO or its fragment detecting DIABLO in a biological sample (by contacting the sample with an IAP and detecting the presence of an IAP/DIABLO complex), modulating the death of a cell (by contacting a cell with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents
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                                                                                                                                                                                                                                                                                                                                                                                             H
                                                                                                                                                                                                                                                                                 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                Isogai T,
, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or hepatic tissue damage associated with a liver disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               partial rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence SEQ ID NO:11570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                    Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.7%;
                                                                                                                                                                                                                                                                                                                                                        Wakamatsu
                                                                                                                                 ed in the specification, abnormality of the prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIABLO.
                                                                                                                                                                                                                                                                                                                                                                              , <sub>1-3</sub>
                                                                                                                                                                      polynucleotides, particularly the the specification, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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Pred. No. 4.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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                                                                                                                                                                                                                                                                                                                                                    Hayashi K,
A, Nagai I
                                                                                                                          the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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                                                                                                                                                                                                                                                                                                                                                    Ά,
                                                                                                                                                                                                                                                                                                                                                    Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                 encoded
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                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an antigen-
                                                                                                                             detection by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                       5602
                                                                                                                                                                                                                                                                                                                                                                                  J;
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Claim 8;

SEQ

ID 11570; 2537pp + CD

ROM; English

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RESULT 14
ABB76208
ABB76208
ABB76208
ABB76208
AC ABB7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                 Novel peptide derived from wild-type human second mitochondria activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76208 standard;
                                      Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-2000; 2000US-0687549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-2001; 2001WO-US32121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIABLO; smac; inhibitor of apoptosis protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human smac (DIABLO) derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                         WPI; 2002-444169/47
                                                                                                                                                                                                                                                                                                       Fesik SW, Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200230959-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
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                                      Page 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKSEPHSLSSEALMRRAVSLVTDST 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKSEPHSLSSEALMRRAVSLVTDST 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "optional C-terminal protecting group"
                               26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                       Betz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No.
                                                                                                                                                                                                                                                                                                       SP,
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                                                                                                                                                                                                                                                                                                    Liu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                    Olejniczak ET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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                                                                                                                                                                                                                                                                                                    Sun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
The invention relates to polynucleotides encoding an Omi (serine protease) peptide or polypeptide. The Omi peptide specifically binds to portion of an Inhibitor of Apoptosis Protein (IAP). The Omi polypeptide induces caspase independent apoptosis, or fails to have serine protease activity. The Omi peptides are useful for regulating or altering apoptosis, specifically caspase-mediated apoptosis, and as immunogens for
                                                                                                                                                                                                                       apoptosis proteins, useful for regulapoptosis and for treating cancer,
                                                                                                                                                                                                                         New Omi nucleic acids and peptides that bind to an inhibitor of apoptosis proteins, useful for regulating or altering caspase-mediated apoptosis and for treating cancer, tumor, or autoimmune diseases .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUL-2001;
14-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omi; HtrA2; serine protease; inhibitor of apoptosis protein; caspase; apoptosis; cytostatic; immunosuppressive; neuroprote
                                                                                                                                                                                                                                                                                                                          WPI; 2003-221760/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vasotropic;
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4.8e-09;
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T15529
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ALIGNMENTS

from GB/EMBL/DDBJ

November 1995 legans cosmid C17C3.

20-Sep-1999 #text_change 20-Sep-1999

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R;Du, 2.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C17C3.
A;Reference number: Z18366
A;Accession: T1531
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                               hypothetical protein C17C3.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
T15531
                                                                                                                   A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-321 <BUZ>
A;Cross-references: EMBL:U41279; NID:g1086905; PID:g1086910; PIDN:AAB52693.1; GSPDB:G
A;Experimental source: strain Bristol N2; clone C17C3
A;Experimental source: strain Bristol N2; clone C17C3
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A; Introns: 45/3; 98/2; 175/2
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A; Residues: 1-313 < DUZ>
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                                        A; Introns: 16/3; 38/3; 53/3; 106/2; 183/2
                                                             A; Map position:
                                                                                A;Gene:
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  Query Match
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                                                                                CESP:C17C3.10
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  37.6%; Score 53;
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Length 321;
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probable membrane protein YML023c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 19-Apr-2002
C;Accession: S49754
R;Badcock, K.; Churcher, C.
submitted to the EMBL Data Library, November 1994
A;Reference number: S49741
A;Accession: S49754
A;Accession: S49754
A;Molecule type: DNA
A;Residues: 1-556 <BAD>
A;Cross-references: EMBL:246659; NID:9575680; PID:9575696; GSPDB:GN00013; MIPS:YML023c
C;Genetics:
A;Gene: MIPS:YML023c
A;Cross-references: SGD:S0004485
A;Cross-references: SGD:S0004485
A;Cross-references: Saccharomyces cerevisiae probable membrane protein YML023c
C;Keywords: transmembrane #status predicted <TM1>
F;482-498/Domain: transmembrane #status predicted <TM1>
F;482-498/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein slr1888 - Synechocystis sp. (strain PCC 6803)
C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C; Accession: S77148
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; A.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada
DNA Res. 3, 109-136, 1996
       hypothetical protein R08D7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #t
                                                            RESULT
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                                                                                                                                                                                                            l Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                     1-630 <KAN>
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12; Conser
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                                                                                                                                PIAQKSEP-----HSLSSEALMRRAVSLVTD 28
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     #sequence_revision
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41.78;
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                                                                                                                                                                                                   Pred. No. 7.4,
6; Mismatches
                                                                                                                                                                                                                            Score 52;
Pred. No.
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7; Mismatches
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Pred. No.
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10-Nov-1995 #text_change 09-Sep-1997
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                                                                                                                                                                                                                                                                                                                                                     translation not shown
                                                                                                                                                                                                                                                                                                                                                                                           PMID:8905231
                                                                                                                                                                                                                                             DB 2;
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y.; Miyajima, N.;
Yamada, M.; Yasuda
                                                                                                                                                                                                     1;
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JC4965
                                                   A; Molecule type: mRNA
A; Residues: 1-429 < GRE>
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                                                                                                                                                                                                                                     elk1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE001984; A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-256 <WHI>
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A; Residues: 1-455 < AIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A; Reference number: S41036
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R; Ainscough,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                     mouse
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38.1%;
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C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 16-Jul-1999
C:Accession: JC4965; 148339; 148340; S54908
C:Accession: JC4965; 148339; T48340; S54908
A;Cross-references: EMBL:X87257; NID:g836634; PIDN:CAA60715.1; PID:g836635
A;Experimental source: embyro
R;Giovane, A.; Pintzas, A.; Maira, S.M.; Sobieszczuk, P.; Wasylyk, B.
                                                                                                               A;Title: Structure and organization of the mouse elkl gene. A;Reference number: JC4965; MUID:97017146; PMID:8863747 A;Accession: JC4965...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-De
C;Accession: E75401
R;White, O.; Eisen, J.A.; Heidelberg, J.F.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: E75401 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 37/3; 128/1; 165/3; 291/2; 357/2; 407/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: The C. elegans genome sequencing project: a beginning A; Reference number: S24457; MUID:92168156; PMID:1538779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein - Deinococcus radiodurans (strain R1)
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5.3;
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7.2;
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, L.; Utterback,
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T.; Zalewski,
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                  nitrogen regulation protein nifR [imported] - C:SpecLes: Agrobacterium tumefaciens C:Date: 11-Jan-2002 #sequence_revision 11-Jan-C:Accession: AD2754 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F20D10.10 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change C:Accession: T05616
                                                                                                                                                                                                                                    RESULT
AD2754
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: F20D10.10
C; Superfamily: retroelement pol polyprotein;
F;146-201/Domain: RING finger homology <RRN>
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A;Experimental source: cultivar Columbia;
C;Genetics:
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A; Residues: 1-720 <BEV>
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A; Accession: T05616
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C:Superfamily: elk-1 transforming protein;
F;7-86/Domain: ets DNA-binding domain homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;MoLecule type: mRNA
A;Residues: 5-132,'T',134-224 <RE2>
A;Cross-references: EMBI.236939; NID:9535922; PIDN:CAA85391.1; PID:9535923
C;Comment: This protein belongs to the subfamily of ternary complex factor
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A;Title: Net, a new ets transcription factor that is activated A;Reference number: A53837; MUID:95047310; PMID:7958835

A;Accession: I48339

A;Accession: I48339
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A; Residues: 1-429 < RES>
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                    AVKAEPEVSASEGLLARLPAILTENT 295
                                                                                                                                                                                                                                                                                                              PVVQKSEPLTPTSAWRAAERLAKVAIMRKHMNRVSD
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          35.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.; Wambutt, R.; Bancroft, I.;
Database, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; I
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                                                                                                                                                                        11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB/EMBL/DDBJ
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3.7;
                                                                                                                                                                                                              Agrobacterium tumefaciens (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone F20D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                              2;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 720;
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                      tumefaciens C58
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                                                                                                                                                                                                              C58,
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T15528
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  Local Similarity
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RESULT 10
B97535
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: B97535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001
C;Accession: B97535
A; Map position: 2
A; Introns: 50/2; 119/2
                                                                                          A; Molecule type: DNA
A; Residues: 1-210 <DUZ>
A; Cross-references: EMBL:U41279;
                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                      C; Species: Caenorhabditis elegans
C; Date: 20-Sep-1999 #sequence_rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
C; Superfamily:
                                    A; Gene: CESP:C17C3.8
                                                                          A; Experimental source:
                                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                       A; Reference number: Z18366
A; Accession: T15528
                                                                                                                                                                                                                                                                                                                               hypothetical protein C17C3.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-338 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: nifR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-338 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: AD2754
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: AGR_C_2661
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                                                        Genetics:
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Best Local
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13; Conserv
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13; Conserv
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                                                                                                                                                                                                                                                                          T15528
                                                                                                                                                                                                                                                                                                                                                                                                                                LPLPELSEPFSIGSVTIRNRAVLAPMSGVTD 36
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                                                                                                                                                                                                                                                                                        #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE007869; PIDN:AAK87235.1; PID:g15156519; GSPDB:GN00169
                                                                          strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome hypothetical protein HI0979
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41.9%;
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    Caenorhabditis elegans

                                                                          79; NID:g1086905; PID:g1086907; Bristol N2; clone C17C3
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Pred. No. 10;
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                                                                                                                                                     GB/EMBL/DDB.
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                                                                                                                                                                                                                cosmid C17C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
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                                                                                              PIDN: AAB52692.1;
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Markelz,
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                                                                                              GSPDB:
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34.0%;

Score Pred.

NO.

2

Length 210;

DB 8.6;

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A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A:Title: Deciphering the biology of Mycobacterium tuberculosis from the A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70663
A:Status: preliminary; nucleic acid sequence not shown; translation not A:Molecule type: DNA
A:Residues: 1-131 <COL>
A:Cross-references: GB:283859; GB:AL123456; NID:g3261678; PIDN:CAB06116...
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Rv1838c
C:Superfamily: conserved hypothetical protein MJ0974
      phosphate uptake
                                                                                                                                                                                                                                                                         C; Superfamily:
                                                                                                                                                                                                                                                                                            A; Map position: 1
A; Introns: 149/3; 301/3
                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-390 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, January 1998 A;Description: Genomic sequence for Arabidopsis thaliana A;Reference number: Z14211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, eologis, A.; Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein kinase homolog F2401.13 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 17-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C;Accession: T01451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Rv1838c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Caccession: F70663
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                      A; Gene: ATSP:F2401.13
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: translated from GB/EMBL/DDB:
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Best Local
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                                                                                                                                                                                          Similarity
9; Conser
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                                                                                                                               KSEPHSLSSEALMRRAVSL 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAQKSEPHSLSSEALMRRAVSLVT 27
                                                                                                                                                                                                                                                                    kinase-related transforming protein; protein kinase homology
      ABC
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      transporter
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H37Rv
      permease
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Pred. No.
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                                                                                                                                                                                                             Pred. No.
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    protein
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25;
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    phoT (imported) -
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Coliveira, R.C.; Palmiteri, R.C.; Palmiteri, R.C.; Matsukuma, A.Y.; Matsukuma, R.C.; de Oliveira, M.A.; Sancelli, R.V.; Sawa A;Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase III subunit xF1807 [imported] - xylella fastidiosa (strain 9a5c) C:Species: Xylella fastidiosa C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C; Superfamily: DNA-directed DNA polymerase III gamma chain
                                                                                                                                                     A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004002; GI
A;Experimental source: strain 9a5c
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A; Residues: 1-608 <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 bel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; anonymous, The xyre Nature 406, 151-157,
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A;Gene: phoT; SMb21174
A;Genome: plasmid
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A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
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A; Residues: 1-505 < KUR>
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S.; Wells, D.H.; Wong, K.
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01-MAR-2003
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P0501G01.22 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8R1D8 PRELIMINARY; PRT; 157 AA.
Q8R1D8;
Q08R1D8;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 0610041612 gene.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024780; AAH24780.1; -.
SEQUENCE 157 AA; 17799 MW; 0F67319F05EAC6E7 CRC64;
   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                   (TremBLrel. 17, Created)
(TremBLrel. 17, Last sequ
(TremBLrel. 23, Last anno
                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                  PRELIMINARY;
(Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.2%;
93.3%;
                                                                                                       Last sequence update)
Last annotation update)

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 130; DB 11;
Pred. No. 2.6e-12;
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                  224
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Best Local S
Matches 12
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Best Local S
Matches 10
                                                                PROSITE; PS50888; HLH
Hypothetical protein.
SEQUENCE 313 AA; 3
                                                                                                              TRANSCRIPTION FACTORS.

EMBL; U41279; AAK31421.1; -.

WormPep; C17C3.7; CE04027.

InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.

SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U1-NOV-1996 (TrEMBLrel. 01, Cr
01-NOV-1996 (TrEMBLrel. 01, La
01-MAR-2003 (TrEMBLrel. 23, La
Hypothetical 36.2 kDa protein.
C17C3.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Virio
Spermatophyta; I
Ehrhartoideae;
                                                                                                                                                                                                  "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (1
                                                                                                                                                                                                                                                                                                                                   Du Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q18054;
01-NOV-1996
                                                                                                                                                                                                                                                       Waterston
                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: investigating biology. The C. elegans Sequenc Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q18054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-cv. Nipponbare; Sasaki T., Matsumoto T., Yamam "Oryza sativa nipponbare(GA3) clone:P0501601.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP002819; BAB21093.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gramene; Q9AX95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω
                                                                                                                                                                                                                                                                                                                 sequence of C. elections itted (DEC-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                             SM00353; HLH; 1.
    Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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PS00037; MYB_1; 1.
224 AA; 23798 MW; FEF94?
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    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peloderinae;
                                                                                          HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=9851916;
                                                                                                                                                                                                                                                                                                                   elegans
() to the
              37.6%;
                                                                36167 MW;
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inae; Caenorhabditis.
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yta; Liliopsida; Poales; Poaceae;
 Score 53; DB Pred. No. 6.1; 3; Mismatches
                                                                                                                                                                                                                                                                                                              cosmid C17C3.";
EMBL/GenBank/DDBJ databases
   Ψ
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                             DCCE0B2DAC63DF99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEF94A53AE500A92 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing
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                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
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 9;
                              Length 313;
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 Indels
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                                                                                                                                                                                                     (BHLH) FAMILY
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0;
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Gaps
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0;
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Q8DF79
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Best Local S
Matches 12
                                                                                                     01-MAR-2003
01-MAR-2003
01-MAR-2003
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Submitted (DEC-
[3]
                                                        Vibrio vulnificus
                                                                         VV10342.
                                                                                                                                                     Q8DF79;
                                                                                                                                                                     Q8DF79
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Q18056;
                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
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01-NOV-1996 (TrEMBLrel. 01, Cr
01-NOV-1996 (TrEMBLrel. 01, La
01-MAR-2003 (TrEMBLrel. 23, La
Hypothetical 37.1 kDa protein.
C17C3:10.
Bacteria; Proteobacteria; Vibrionaceae; Vibrio. NCBI_TaxID=672;
                                                                  Cytosine/adenosine
                                                                                                                                                                                                                                                                                                                                                               EMBL; U41279; AAK31423.1; -.
WormPep; C17C3.10; CE044330.
InterPro; 1PR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2001) to -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. el
investigating biology. The C. elegans
crience 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DEC-1995)
                                                                                                                                                                                                                                                                                                                          321 AA;
                                                                                 (TrEMBLrel.
                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9851916;
                                                                     deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elegans
) to the
                                                                                                                                                                                                                                                                                                                           37103 MW;
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                                                                                                                                                                                                                                                                              37.6%;
                                                                                 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  the EMBL/GenBank/DDBJ databases TO THE BASIC HELIX-LOOP-HELIX (
                          Gammaproteobacteria;
                                                                               Created)
Last sequence up
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Last annotation updat
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Last sequ
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                 Score 53; I
Pred. No. 6.
                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                        7F3B63AA7549A1CD CRC64;
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                                                                                                                                                                                                            119
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Sequencing Consort
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6.3;
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                                                                                              update)
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                                                                               update)
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                          Vibrionales;
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                                                                                                                                                                                                                                                                                            Length 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BHLH)
                                                                                                                                                                                                                                                                 0;
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RESULT
Q8DD72
ID Q8DD72
ID Q8
AC Q8

        PT 3661
ID 3661
ID P7
AC P7
DT 011
DT 011
DT 011
DT 011
DT 01
DT 01
EN SY
GN SL
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Matches 10
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Best Local :
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01-MAR-2003 (TIEMBLI
01-MAR-2003 (TIEMBLI
Putative threonine
                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura T.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K., Okumura (M.)

Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Yamada M., Yasuda M.,

Matanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P73661
P73661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, C
01-FEB-1997 (TrEMBLrel. 02, L
01-MAR-2003 (TrEMBLrel. 23, L
Hypothetical protein slr1888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AE016800; AA009612.1; -
Complete proteome.
SEQUENCE 207 AA; 21859 MW; ADA3B5E7F57E14E2 CRC64;
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Choy H.E.;
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                                             Shimpo S., Takeuchi C., Tabata S.;
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Brinkman F.S., Schoofs G., Hancock R.E., De Mot R.;
"Influence of a putative BCF sigma factor on express
outer membrane protein, OprF, in Pseudomonas aerugii
pseudomonas fluorescens.";
J. Bacteriol. 181:4746-4754(1999).
EMBL; AF027290; AAD11567.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to active BCR-related gene.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                      Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases EMBL; BC042307; AAH42307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL; D90908; BAA17706.1; -.
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                           Putative
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InterPro; IPR000182; GCN5acetyltransf.
                                                                                                    MEDLINE=99369842; PubMed=10438740;
                                                                                                                        STRAIN-PAO1;
                                                                                                                                                                        NCBI_TaxID=287;
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01-MAY-2000
01-MAR-2002
                                                                                                                                                                                                  MEDLINE=20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Pet White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Pet Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richar Dodson R.J., Haft D.H., Gwinn M.L., Pamphile W., Crosby M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zal Makarova K.S., Aravind L., Daly M.J., Minton K.W., Flei
                                   radiodurans Rl.";
Science 286:1571-1577(1999).
EMBL; AE001984; AAF10959.1;
                                                                                                                                                      Ketchum K.A., Nelson
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=R1
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Deinococcus-Thermus; Deinococcaceae; Deinococcus. NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein DR1380.
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Vibrionaceae; Vibrio.
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              DR1380;
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n DR1380.
                                                                                                                                                                          nd L.,
K.E.,
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h H.O., Venter J.C.,
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by M., Shen M.,
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Mayer K.F.)
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O1-MAR-2003 (TTEMBLrel. 23, Last
Hypothetical 79.2 kDa protein.
F20D10.10 OR AT4G37890.
                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FING
EMBL; AL03538; CAB37529.1; -.
EMBL; AL103538; CAB37529.1; -.
EMBL; AL101592; CAB80454.1; -.
Interpro; IPR0003841; Znf_ring.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Bevan M., Wedler H., Kutzner M.,
Mayer K.F.X., Schueller C.;
Submitted (FEB-1999) to the EMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                         PROSITE; PS50089; ZF_RING_2; 1.
Hypothetical protein; Metal-binding;
SEQUENCE 720 AA; 79166 MW; 8E910
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 PRELIMINARY;
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    Q8EUZ4;
01-MAR-2003
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ish
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
"Arabidopsis thaliana full-length cDNA.";
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AT4G37880/F20010_10.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Genew; HGNC:14004; C11orf25.
Hypothetical protein.
SEQUENCE 981 AA; 114654 M
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE 739 AA; 81406 MW; 6F6949CACB24AE1C CRC64;
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                                                                                          Q8EUZ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thesis (1996), Department of Human Paris, France.
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EMBL; APO04173; BAC44567.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 1003 AA; 109261 MW; 0C2AFF329CII
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Yoshino C., Horino A., Shiba T., Sasal
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US-09-413-814-5
US-09-142-648-8
US-09-155-396-4
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US-09-252-991A-28715
US-09-342-648-4
US-09-342-648-2
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RESULT 1 US-09-479-309-2 Sequence 2, A Patent No. 61 GENERAL INFOR APPLICANT: W APPLICANT: W TITLE REFEREN FILE REFEREN CURRENT APPL		45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	
SULT 1 -09-479-309-2 Sequence 2, Application US/0947 Patent No. 6110691 GENERAL INFORMATION: APPLICANT: Wang, Xiaodong APPLICANT: Wang, Xiaodong TITLE OF INVENTION: Activators FILE REFERENCE: UTSD0630 CURRENT APPLICATION NUMBER: US.		40	40	40	40	40	40	40	40.5	40.5	40.5	40.5	41	41	41	41	41	41	41	
-2 Application US/09479309 6110691 FORMATION: Wang, Xiaodong Du, Chunying NVENTON: Activators of DENCE: UTSD0630 PLICATION NUMBER: US/09/		28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.7	28.7	28.7		29.1	29.1	29.1	29.1	29.1	29.1		
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ULT 1 09-479-309-2 equence 2, Application US/09479309 atent No. 6110691 ENERAL INFORMATION: APPLICANT: Wang, Xiaodong APPLICANT: DL, Chunying TITLE OF INVENTION: Activators of Caspases FILE REFERENCE: UTSD0630 CURRENT APPLICATION NUMBER: US/09/479,309	ALIGNMENTS	US-09-252-991A-26360	US-09-252-991A-29849	US-09-198-452A-1006	US-09-252-991A-28433	US-09-252-991A-18834	US-09-347-650-8	US-09-252-991A-31261	US-09-198-452A-1124	US-09-293-273-7	US-09-134-596-7	US-08-861-269-7	PCT-US94-00198-4	US-09-252-991A-23210	US-09-342-648-6	US-09-198-452A-7	US-09-252-991A-29621	US-09-107-532A-5791	US-09-252-991A-31686	
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CURRENT FILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN VEr. 2.1

SEQ ID NO 2

LENGTH: 239

TYPE: PRT

ORGANISM: human
US-09-479-309-2
                                                                                          APPLICANT: Wang, Xiaodong
APPLICANT: Du, Chunying
TITLE OF INVENTION: Activators of Caspases
FILE REFERENCE: UTSD0630
CURRENT APPLICATION NUMBER: US/09/627,393
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 09/479,309
PRIOR APPLICATION NUMBER: 09/479,309
PRIOR FILING DATE: 2000-01-06
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LENGTH: 239
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09627393 Patent No. 6534267 GENERAL INFORMATION:
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Best Local Similarity
Matches 30; Conserva
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100.0%; Pred. No. 1.2e-1
tive 0; Mismatches
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Query Match

100.0%;

Score 141;

DB 4;

Length 239;

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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                          APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide of INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER APPLICATION NUMBER: DE 198 46 93.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOUTWARE: PatentIn Ver. 2.1
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LENGTH: 198
                                    Query Match
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Matches
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                                                                                  LENGTH: 899
TYPE: PRT
ORGANISM: Sorangium cellulosum
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     Local Similarity hes 10; Conserv
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30; Conserv
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Brandt, Petra
Cino, Paul M
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Conservative
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; Score 44.5; D; Pred. No. 88; 9; Mismatches
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Pred. No.
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US-09-252-991A-24435

; Sequence 24435, Application US/09252991A

; Patent No. 6551795
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; ORGANISM: S.
US-09-165-396-4
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Best Local Similarity
Watches 9; Conserve
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US-09-342-648-8
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LENGTH: 799
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1169-B
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/165,396
CURRENT FILING DATE: 1998-10-02
EARLIER APPLICATION NUMBER: PCT/US98/02332
EARLIER FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: 60/037,859
EARLIER FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ISOLATED CANDIDA ALBICANS OLIGOPEPTIDE TRANSPORTER GENE FILE REFERENCE: 372.6520P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BECKER, JEFFREY W. APPLICANT: LUBKOWITZ, MARK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
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CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,659
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Triticum aestivum
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29.5%;
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                                                                      Matches
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Best Local
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 147
                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GALLO, Gregory J.
TITLE OF INVENTION: APOPTOSIS ASSOCIATED PROTEIN BBK
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 29-MAY-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                   Local Similarity
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109 PSPELQGPPSTEKEAILRRLVALLEE 134
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                                 PIAQKSEPHSLSSEALMRRAVSLVTD 28
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                                                                                                                                                                                                                             249 amino acids
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--- TD NO: 11:
                                                                     Conservative
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                                                                                   30.5%;
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                                                                                   Score 43; DB
Pred. No. 29;
                                                                     Mismatches
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US-09-188-177-11
                                     ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-28715
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-28715
                                                                                                                                                                                                                                                                                                                                                   Patent No. 6551795
GENERAL INFORMATION:
                                                                                                SEQ ID NO 28715
LENGTH: 327
                                                                                                                                                                                                                                                                                                                                                                            Sequence 28715, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Appli
Patent No. 6057132
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 1999-02-
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                            APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202)942-8484
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (202)942-8459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: WIXON, Henry N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: APOPTOSIS ASSOCIATED PROTEIN NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: WIXON, Henry N. REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/188,177 FILING DATE: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 30.5%;
Local Similarity 34.6%;
es 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202)942-8484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s: single
linear
                                                                                                                                                                                                                                                                               107196.136
                                                                                                                                                                                             1998-02-18
30.5%;
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  Score 43;
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Pred. No. 29;
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  DB 4;
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  Length 327;
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Best Local Similarity
Watches 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Oryza sativa US-09-342-648-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-342-648-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 199-06-29
EARLIER APPLICATION NUMBER: 60/092,659
EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09342648 Patent No. 6248584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cahoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1169-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 36
TYPE: PRT
                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILLING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
                   FILING DATE: 16-FEB-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHOR
TITLE OF INVENTION: THE TREATMENT AND DIAGN
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                 APPLICATION NUMBER:
                                                                                                                                 CLASSIFICATION:
                                                                                                                                              APPLICATION NUMBER: US/08/826,246 FILING DATE: 28-MAR-1997
                                                                                                                                                                                              COMPUTER: IBM CO
OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369
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                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                            FastSEQ Version 2.0
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52.9%;
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Pred. No.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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49;
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                               US-08-944-495-2
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US-08-944-495-2
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                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protei
                                             MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                     NAME: COTIZZÍ, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-078-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790909
TELEPAX: (212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                       LENGTH:
                                                                             TOPOLOGY:
                                                                                        TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                          TELEFAX: (212)8699741
TELEX: 66141 PENNIE
                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PENNIE & EDMONDS LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)86997.
TELEX: 66141 PENNIE
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5. 6087477
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10036-2711
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Similarity 43.5%;
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                                                                                                                                                                                                         (212)7909090
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internal
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internal
                                                                                           unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARDIOVASCULAR DISEASE
30.5%;
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Pred. No.
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Mismatches

0;

Gaps

0

DB 3;

Length 570; Indels

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EARLIER APPLICATION NUMBER: 08/870,434
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 08/799,910
EARLIER FILING DATE: 1997-02-13
EARLIER FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 570
TYPE: PRT
ORGANISM: Homo sapiens
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US-08-925-588-2
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US-09-126-640-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08925588
Patent No. 6221628
GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
THE TREATMENT AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FALB, Dean A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Applic Patent No. 6099823
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/925,588

FILING DATE: 08-Sep-1997

CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:

APPLICATION UMBER: 08/799,910

FILING DATE: <URKNOWN>
ATTORNEY/AGENT INFORMATION:

NAME: COTUZZÍ, LAURA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 KSHPEVLIAEALAANAGALITST 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KSEPHSLSSEALMRRAVSLVTDS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                    STREET: 1155 AV
CITY: New York
STATE: NY
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                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PENNIE & EDMONDS LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09126640A
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43.5%;
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4; Mismatches
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Search completed: October Job time : 26 secs
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                                                                                                                     Best Local Similarity 43.5
Matches 10; Conservative
                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (212)7909090
                                                          451 KSHPEVLIAEALAANAGALITST 473
                                                                                       KSEPHSLSSEALMRRAVSLVTDS 29
                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
                                                                                                                                                                                                                                                                                        ENGTH: 570 amino acids
                                                                                                                                  30.5%;
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              2003, 09:40:40
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Pred. No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     Query
Match
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   PIR_76:*
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pir2:*
pir3:*
pir4:*
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cytochrome P450 HL
H+transporting tw
dystrophin - rat (
hypothetical prote
ubiquinol-cytochro
sex pheromone inhi
probable catalase
cathepsin G (EC 3.
ZF3 domain - human
hypothetical MTCO1
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interferon alpha (probable membrane hypothetical prote pepsin A (EC 3.4.2 ceratotoxin A - Me
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ATPase R1 subunit
ATP synthase beta-
amyloid protein AL
hypothetical prote
fibronectin recept
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Query Match 24.8%; Score 35; DB 2; Length 23; Best Local Similarity 53.3%; Pred. No. 68; Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps Qy 15 SEALMRRAVSLVTDS 29	RESULT 2 151922 Cystic fibrosis transmembrane conductance regulator - rabbit (fragment) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Dacte: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Aug-1999 C;Accession: 151922 R;McGrath, S.A.; Basu, A.; Zeitlin, P.L. Am. J. Respir. Cell Mol. Biol. 8, 201-208, 1993 A;Title: Cystic fibrosis gene and protein expression during fetal lung deve A;Reference number: 151922; MUID:93152187; PMID:7678968 A;Accession: 151922 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-23 <mcgs a;cross-references:="" atp-bin<="" c;superfamily:="" conductance="" cystic="" fibrosis="" gb:s54552;="" nid:g265093;="" pid:g265094="" pidn:aab25301.1;="" regulator;="" th="" transmembrane=""><th>RESULT 1 T48881 Ieader peptide [imported] - Vibrio sp. C:Species: Vibrio sp. C:Species: Uriorio sp. C:Species: Vibrio sp. C:Glansdorf C:Glansdorf A:Species: Vibrio sp. C:Glansdorf A:Species: Vibrio sp.</th><th>30 25 17.7 29 2 B61613 21 25 17.7 30 2 S07217 22 4.5 17.4 23 2 A59480 23 24.5 17.4 25 2 PC4445 24 17.0 12 1 A43975 36 24 17.0 18 2 S55002 27 17.0 20 2 H28949 28 17.0 21 2 A35646 29 24 17.0 21 2 A35646 39 24 17.0 21 2 A35646 39 24 17.0 21 2 A35646 41 24 17.0 25 2 PO3369 41 27 0 25 2 PO3369 41 27 0 25 2 PO3369 42 17.0 26 2 B24753 43 24 17.0 26 2 B44753 44 27 17.0 27 2 T13836 45 24 17.0 27 2 T13836 46 27 17.0 27 2 T13836 47 28 AALIGNMENTS</th></mcgs>	RESULT 1 T48881 Ieader peptide [imported] - Vibrio sp. C:Species: Vibrio sp. C:Species: Uriorio sp. C:Species: Vibrio sp. C:Glansdorf C:Glansdorf A:Species: Vibrio sp.	30 25 17.7 29 2 B61613 21 25 17.7 30 2 S07217 22 4.5 17.4 23 2 A59480 23 24.5 17.4 25 2 PC4445 24 17.0 12 1 A43975 36 24 17.0 18 2 S55002 27 17.0 20 2 H28949 28 17.0 21 2 A35646 29 24 17.0 21 2 A35646 39 24 17.0 21 2 A35646 39 24 17.0 21 2 A35646 41 24 17.0 25 2 PO3369 41 27 0 25 2 PO3369 41 27 0 25 2 PO3369 42 17.0 26 2 B24753 43 24 17.0 26 2 B44753 44 27 17.0 27 2 T13836 45 24 17.0 27 2 T13836 46 27 17.0 27 2 T13836 47 28 AALIGNMENTS
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RESULT 4
$00347
triacylglycerol lipase (EC 3.1.1.3) - bovine (fragment)
N;Alternate names: hormone-sensitive lipase
C;Specles: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 30-Sep-1993
C;Accession: $00347
R;Garton, A.J.; Campbell, D.G.; Cohen, P.; Yeaman, S.J.
FEBS Lett. 229, 68-72, 1988
A;Title: Primary structure of the site on bovine hormone-sensitive lipase phosphorylated A;Reference number: $00347; MUID:88152238; PMID:3345839
A;Accession: $00347
A;Molecule type: protein
A;Residues: 1-27 GAR>
C;Comment: Activation of this enzyme involves phosphorylation of Ser-8 by cyclic AMP-dep C;Superfamily: hormone-sensitive lipase
C;Superfamily: hormone-sensitive lipase
F;8/Binding site: phosphate (Ser) (covalent) #status experimental
F;10/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                class I histocompatibility antigen H-2K(d) alpha chain, alternate splice form C; Species: Mus musculus (house mouse)
C; Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 07-May-1999
C; Accession: A60897
R; Abu-Hadid, M.M.; Fuji, H.; Sood, A.K.
Mol. Immunol. 25, 739-749, 1988
A; Title: Identification of an alternatively spliced K(d) and the Qa-6(d) mRNAs A; Reference number: A60897; MUID:89039921; pMID:3141798
                                                                           A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-20 <ABU>
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A60897
                                                                                                                                      A; Reference number: A60897; A; Accession: A60897
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C;Species: Thermus aquaticus
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: S00901
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A; Residues: 1-15 <CRO>
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Score 29; DB
Pred. No. 4.9e
4; Mismatches
   4;
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Pred. No. 2.4e+02
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Pred. No.
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4.9e+02;
hes 5;
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A; Molecule type:
A; Residues: 1-20
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interferon alpha (component i) - human (fragment)
(;Species: Homo sapiens (man)
(;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Mar-1999
C;Accession: G42753
R;Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.;
J. Biol. Chem. 267, 15210-15216, 1992
A;Title: Purification and characterization of multiple components of human lymphoblas
A;Reference number: A42733; MUID:92340576; pMID:1634550
A;Accession: G42753
                                   C;Accession: A60728
R;Pineau, T.; Galtier, P.; Bonfils, C.; Derancourt, J.;
Biochem. Pharmacol. 39, 901-909, 1990
A;Title: Purification of a sheep liver cytochrome P-450
A;Reference number: A60728; MUID:90179800; PMID:2310415
A;Accession: A60728
                                                                                                                                                           C;Species: Ovis sp. (sheep)
C;Date: 14-May-1993 #sequence_revision 14-May-1993
                                                                                                                                                                                                cytochrome P450 3A, troleandomycin-induced - N; Contains: oxidoreductase (EC 1.-.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 1-18 <200>
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C; Keywords: ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 1-28 <CIA> C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Claccio, P.J.; Halpert, J.R.
Arch. Biochem. Biophys. 271, 284-299, 1989
A;Title: Characterization of a phenobarbital-inducible (A;Reference number: S04341; MUID:89271912; PMID:2786372
A;Accession: S04341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Date: 28-Fe
C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytochrome P450 PBD-1 - dog (fragment)
N;Alternate names: cytochrome P450 A
N;Contains: oxidoreductase (EC 1.-.-)
C;Species: Canis lupus familiaris (dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CYP3A
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Best Local
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8; Conserv
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protein
PIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                        19.18;
44.48;
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46.7%;
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No.
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8.9e+02;
3;
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                                                                                                                     J.; Maurel,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
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P450 isozyme is a member of the P450IIIA family

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is not Thu Oct

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RESULT
C48186
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A30323
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Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP syntha A;Reference number: A48186; MUID:93317598; PMID:8327463
A;Accession: A48186
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C;Genetics:
A;Gene: CYP3A
C;Superfamily: human cytoch
C;Keywords: electron transf
amyloid protein AL (Ig lambda chain V region) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change
C;Accession: A30323
                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-23 <DE1>
A; Residues: 1-23 <DE1>
A; Experimental source: pollen
A; Note: sequence extracted fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Nicotiana sylvestris (wood tobacco)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A48186
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A48186
ATP synthase beta-1 chain - wood tobacco (fragment)
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A; Residues: 1-22 < DELY
A; Experimental source: pollen
A; Note: sequence extracted from
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C:Species: Nicotiana sylvestris (wood tobacco)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
C:Accession: C48186
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nes 6; Conserv
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Pred. No.
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2; Mismatches
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               21-Feb-1990 #text_change 16-Aug-1996
                                                                                                                                                                                                                                     No. 1.2e+03;
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le+03;
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heme; monooxygenase;
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RESULT 13
A37825
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RyJohnson, D.; Gattung, s.
Submitted to the EMBL Data Library, Novemb
                                                                                                                                                                                                                                                  fibronectin receptor alpha chain - chicken (fragment)
c;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 18-Jun-1993
C;Accession: A37825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein K09E3.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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T29626
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В
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A;Title: Systemic senile amyloidosis. Identification of a
                                                                                                                                                                         A; Reference number: A37825; A; Accession: A37825
                                                                                                                                                                                        A; Title: Identification and characterization of a dimeric chicken fibronectin recepto A; Reference number: A37825; MUID:90354452; PMID:2143763
                                                                                                                                                                                                                    R;Hofer, U.; Syfrig, J.; Chiquet-Ehrismann, J. Biol. Chem. 265, 14561-14565, 1990
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Best Local :
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5 TQPHSVS 11
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PFAFRGSPGSLFGFAL
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Pred. No. 1.4e+03;
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RESULT 14

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cytochrome P450 HLp3 - human (fragment)
N;Contains: oxidoreductase (EC 1.-.-)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-193 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999
C;Date: 17-Apr-193 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999
C;Accession: A60558
R;Wrighton, S.A.; Ring, B.J.; Watkins, P.B.; Vandenbranden, M.
Mol. Pharmacol. 36, 97-105, 1989
A;Title: Identification of a polymorphically expressed member of the human cytochrome P-A;Reference number: A60558; MUID:89313723; PMID:2747634
A;Accession: A60558
A;Molecule type: protein
A;Residues: 1-29 <WRID
C;Comment: This protein strongly resembles, but is distinct from, cytochrome P450 CyP3A5
C;Superfamily: human cytochrome P450 CyP3A5; cytochrome P450 homology
C;Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A43768
Hu-like protein HB1 - Bifidobacterium longum (fragment)
C;Species: Blfidobacterium longum
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 16-Feb-1997
C;Accession: A43768
R;Goshima, N.; Kano, Y.; Imamoto, F.
Biochimie 72, 207-212, 1990
A;Title: Characterization of HU-like protein from Bifidobacterium longum.
A;Reference number: A43768; MUID:90344917; PMID:2116910
A;Accession: A43768
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-27 <GOS>
C;Keywords: DNA binding
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Search completed: October 2, 2003, 09:43:21 Job time : 19 secs
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    Mismatches

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20 kDa neutrophil cationic protein (NCP) (Fra
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ENZYME REGULATION: RAPIDLY ACTIVATED BY CAMP-DEPENDENT PHOSPHORYLATION UNDER THE INFLUENCE OF CATECHOLAMINES. DEPHOSPHORYLATION AND INACTIVATION ARE CONTROLLED BY INSULIN. PARHWAY: HORMONE SENSITIVE LIPASE CATALYZES THE RATE LIMITING PARHWAY: HORMONE SENSITIVE LIPASE CATALYZES THE RATE LIMITING STEP IN TRIGLYCERIDE LIPOLYSIS.
                                                                                                            Arch. Allergy
CER 25
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; IPR002168; Lipolytic_enzyme.
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                                                                                                                                                                                 porcine cationic
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                                            DB 1;
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9;
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                         .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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                                          Length 25;
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    Indels
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                                                                                                                                                                                   eosinophil
                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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Gaps
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RESULT 4
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UP35_U
ID UP35_U
AC P82042
DT 30-MAY
DT 15-SEP
CC -!-SU
CC
        RESULT 5
FOR1_MYRGU
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Best Local
                                                                                                                                                                                            TISSUE=Hemolymph;

MEDLINE=98165787; PubMed=9497332;

Mackintosh J.A., Veal D.A., Beattie A.J.,

Mackintosh J.A., Veal D.A., Beattie A.J.,

"Isolation from an ant Myrmecia gulosa of

O-glycosylated proline-rich antibacterial
O-glycosylated proline-rich antibacterial
J. Biol. Chem. 273:6639-6143(1998).

J. Biol. Chem. 273:6639-6143(1998).

HAS A
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"New antibiotic uperin peptides from the dorsal glands of the australian toadlet Uperoleia mjobergii.";

Aust. J. Chem. 49:1325-1331(1996).

-!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, I.INNOCUA, M.LUTEUS, S.AUREUS, P.MULTOCI, S.EPIDERMIS AND F. TREATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myrmecia gulosa (Red bulldog ant).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UP35_UP
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Myrmeciinae; Myrmecia.
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15-DEC-1998 (Rel.
30-MAY-2000 (Rel.
        Antibiotic;
                                                                              -!- INDUCTION: By bacterial infection.
-!- PTM: O-LINKED GLYCAN CONSISTS OF A
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND CARBOHYDRATE-LINKAGE
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=36170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Formaecin 1.
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15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: Expressed by the sl-
-i- MASS SPECTROMETRY: MW=1779; METHOD=FAB
Amphibian defense peptide; Antibiotic; Amio
MOD_RES 17 17
AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uperoleia mjobergii (Australian toadlet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR1_MYRGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amphibia; Batrachia;
Myobatrachinae; Upero
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=104954;
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30-MAY-2000 (Rel.
15-SEP-2003 (Rel.
                        PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY. SIMILARITY: TO DROSOPHILA DROSOCIN.
                                                                                                                                                         FUNCTION: ANTIBACTERIAL PEPTIDE. HAS BUT NONE AGAINST OTHER GRAM-NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Secreted.
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5; Conser
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(Rel. 39, Last sequence update)
(Rel. 42, Last annotation update)
Glycoprotein;
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37, Last sequence 39, Last annotations.
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Last annotation updat
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        Insect
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4; Mismatches
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immunity; Hemolymph
                                                                                                                                                                                                                                                                                                                                                                   SITE
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                                                                                                                                                         ACTIVITY AGAINST E.COLI
BACTERIA AND GRAM-POSITIVE
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                                                                                                                                                                                                                               two inducible
peptides.";
                                                                                                                                                                                                                                                                                  Gooley A.A.;
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RESULT 6
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01-AUG-1992 (Rel. 2
15-SEP-2003 (Rel. 4
ATP synthase alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nono M., Satoh H., Okabe Y., Abe Y., Nakayama K., Okada M.;
"Nucleotide sequence of the large subunit of
ribulose-1,5-bisphosphate carboxylase/oxygenase from the green alga
Bryopsis maxima.";
                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol.
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                                                                                                                                                                                                                         ATP-binding; Hydrolase; Hydrogen ion
                                                                                                                                                                                                                                              PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
ATP synthesis; Chloroplast; Thylakoid; Membrane;
                                                                                                                                                                                                                                                                                                                                           EMBL; x55877; CAA39362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91355942; PubMed=1884001;
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                                                                                                                                                                                                                                                                                              InterPro; IPR000194; ATPase_a/bcentre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SÜBÛNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
SIMILARITY: Belongs to the ATPase alpha/beta chains family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H(+)(Out).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT
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                                                                                                                                                                                                                                                                                                                      S17432;
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                                                                                     Similarity 6; Conser
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                                      IAQKSEPHSLSSEALMRRAV
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PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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23; Last sequence update)
42, Last annotation update)
4 chain (EC 3.6.3.14) (Fragment).
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                                                                                                                                                                                3308 MW;
                                                                                                           18.4%;
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44.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26;
Pred. No.
                                                                                                             Score 26;
Pred. No.
                                                                                     Pred. No. 1.1; Mismatches
                                                                                                                                                                                A25A0BAD077F338B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O-LINKED (GALNAC. ..).
80CEA3AABBC2EOAE CRC64;
21
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                                                                                                                                                                                                                         transport.
                                                                                 . 1.1e+03;
9;
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5.2e+02;
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                                                                                                                              Length 29;
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(1). CF(0)
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ALD DO SON BETT THE REPORT OF THE PROPERTY OF 
  RESULT 8
SODE_PASPI
ID SODE_P
AC P81527
DT 15-DEC
DT 15-DEC
DT 28-FEB
GN SOBE-PASTE
GN SUPETO
GN NCBI_T
RN [1]
RN [1]
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RA BARNES
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-BOLZEVIA, NO. Yaffe D.;
Nudel U., Robzyk K., Yaffe D.;
"Expression of the putative Duchenne muscular dystrophy gene "Expression of the prain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMD
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01-OCT-1989
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  STRAIN≃MT1415;
MEDLINE≖99173752;
Barnes A.C., Bale
                                                                                                                                                                         Pasteurella piscicida (Photobacterium damsela (subsp. piscicida)). Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003
                                                                               SEQUENCE.
                                                                                                                           NCBI_TaxID=38294;
                                                                                                                                                     Vibrionaceae;
                                                                                                                                                                                                                                                    Superoxide
                                                                                                                                                                                                                                                                                                                                                      SODF_PASPI
P81527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-88122671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasma membrane
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co; IPR001589; Actbind_actnin.

co; IPR001202; WW_RSp5_WWP.

E; PS00019; ACTININ_1; PARTIAL.

E; PS00020; ACTININ_2; PARTIAL.

E; PS01159; WW_DOMAIN_1; PARTIAL.

E; PS01159; WW_DOMAIN_1; PARTIAL.
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(Rel. 12, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
     Balebona
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                                                                                                                                                       Photobacterium
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PubMed=10075430;
oona M.C., Horne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=3340214;
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3289 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.4%;
31.6%;
                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
[Fe] (EC 1.15.1.1) (Fragment).
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       Horne M.T.,
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Pred. No.
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       Ellis A.E.;
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RESULT 10
RECX_AZOVI
ID RECX_A
AC P37863
DT 01-OCT
DT 01-OCT
DT 28-FEB
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LEGULTH
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. Golden Harvest, and cv. Prof. Blaau MEDLINE-941/1801; PubMed=8125993;
MO H., van Damme E.J.M., Peumans W.J., Goldste "Isolation and characterization of an N-acetyl-D-galactosamine-binding lectin from D recognizes the blood group A disaccharide (Gal J. Biol. Chem. 269:7666-7673(1994).

-1- FUNCTION: GAL / GALNAC-SPECIFIC LECTIN. AG AND TRYPSIN-TREATED RABBIT ERYTHROCYTES BU IRRESPECTIVE OF BLOOD GROUP TYPE.
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Best Local :
P37863;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last seq.
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
N-acetyl-D-galactosamine-binding lectin subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding lectin subunit B) (Fragment). Iris hollandica (Dutch iris). Eukaryota; Viridiplantae; Streptophyti
                                                                                            RECX_AZOVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Iron.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: DISULFIDE-LINKED
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5; Conserv
                                                                                                                                                                                                                                               LSSEALMR 20
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                                                                                                                                                                                                                                                                                                                                                                                20 AA;
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                                                                                                                                                                                                                                                                                             Conservative
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                                                                                            STANDARD;
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2246 MW;
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                                                                                                                                                                                                                                                                                                                17.7%; 62.5%;
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50.0%;
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    Last sequence update)
Last annotation updat
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oles in resistance to reactive oxygen species.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Periplasmic.
O THE IRON/MANGANESE
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Pred.
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liliopsida;
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                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                       A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GalNAc
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BUT NOT HUMAN
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RESULT
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Best Local S
Matches 6
                                                                                                                   Tejera M.L., Villalba M., Batanero E., Rodriguez R.; "Identification, isolation, and characterization of Ole e allergen of olive tree pollen.";
J. Allergy Clin. Immunol. 104:797-802(1999).
                                                                                                                                                                                                                                                                SEQUENCE (VARIANTS A AND B), TISSUE=Pollen;
                                                                                                                                                                                                                                                                                                                                                         Olea europaea (Common olive).
Eukaryota; Viridiplantae; Etteptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; lamiids; Lamiales; Oleaceae; Olea.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ALL7_OLEEU STANDARD; PRT; 21 AA. P81430; 30-MAY-2000 (Rel. 39, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Pollen allergen Ole e 7 (Ole e VII) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLEEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as l
                                                                                                                                                                                                                                       MEDLINE=99449676;
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4146;
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NON_TER 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 22:1313-1314(1994).

-!- FUNCTION: Modulates recA activity (By similarity).

-!- SUBCELULAR LOCATION: Cytoplasmic (Potential).

-!- SIMILARITY: BELONGS TO THE RECX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S96898; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 113:47-53(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venkatesh T.V., Das H.K.;
"The Azotobacter vinelandii recA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Regulatory RECX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulation of expression.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION
POLYMORPHISM: Many isoforms of the allergen exist due to polymorphism. They can be classified as isoforms of type A (showners) and isoforms of type B. A microheterogeneity is detected a positions 4 and 11 of isoforms of type B.

MISCELLANEOUS: Allergen from olive pollen. Important in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LSSEALMRRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                          PubMed=10518824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2111 MW;
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Pred. No.
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                                                                                                                                                                                                                                                                                         SPECTROMETRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence analysis
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                    Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R., Tettelin H., Dodson R.J., Durkin S., Kolonay J., Madupu R., Nelson W., Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W., Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.; "Role of mobile DNA in the evolution of vancomycin-resistant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _ENTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
NON_TER
SEQUENCE
                                                                                                                                                                                                                       Science 299:2071-2074(2003).

Science 299:2071-2074(2003).

-!- FUNCTION: ACTS AS A COMPETITIVE INHIBITOR OF THE

-!- SUBCELLULAR LOCATION: Secreted (Probable).

-!- MISCELLANEOUS: IAD1 APPEARS TO BE A COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91261999; PubMed-2128961;
Clewell D.B., Pontius L.T., An F.Y., Ike Y., Suzuki A., Nakayama
"Nucleotide sequence of the sex pheromone inhibitor (iAD1)
determinant of Enterococcus faecalis conjugative plasmid pAD1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
 CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAD OR EFA0005.1
                                                        EMBL; AE016833;
PIR; A37391; A37
                                                                                                            entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                   use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                           Enterococcus faecalis."
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-V583 / ATCC 700802; PLASMID-PTEF1; MEDLINE-22550857; PubMed-12663927;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid 24:156-161(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pTEF1, and Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis (Streptococcus faecalis).
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1351;
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                           PROPEP
                                      Plasmid.
                                                                                     EMBL; M62888; AAA98039.1;
                                                  IGR; EFA0005
                                                                                                                                                                                                                 SEQUENCE.
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5 5 5
10 10 10
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31.6%;
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POTENTIAL.

SEX PHEROMONE INHIBITOR DETERMINANT DOEAEBDF1BCD9D08 CRC64;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                          There are no restrictions on
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01-JUN-1994
01-FEB-1996
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NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a chaperonin in a moth, Heliothis virescens.";
J. Mol. Biol. 214:407-422(1990).
1- FUNCTION: IMPLICATED IN MITGCHONDRIAL PROTEIN IMPORT AND
MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF
IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE
REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED
Ceratitis capitata (Mediterranean fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Ins
Neoptera; Endopterygota; Diptera; Brachycera;
Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90339485; PubMed=1974308;
Miller S.G., Leclerc R.F., Erdos G.W.;
"Identification and characterization of a testis-specific isoform of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heliothis virescens (Noctuid moth) (Owlet moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
60 kDa chaperonin, mitochondrial (P60) (Fragm
                                                                                                                                                                                                             CERB_CERCA
P36191;
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                                                                                                                      Ceratotoxin
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PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
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30.8%;
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Pred. No. 1
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                        Brachycera;
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                                                Insecta; Pterygota;
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DE 50S r
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Best Local Similarity
Matches 6; Conserv
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Best Local S
Matches 4
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MEDLINE=79045279; PubMed=152199;

MEDLINE=79045279; PubMed=152199;

Smith N., Willick G., Nazar R.N.;

Smith N., Watheson A.T., Yaguchi M., Willick G., Nazar R.N.;

The 5-S RNA-protein complex from an extreme halophile,

Halobacterium cutirubrum. Purification and characterization.";

Eur. J. Biochem. 89:501-509(1978).

LIST SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       P05970;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
50S ribosomal protein L18P (HCUL18) (HL13) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HALCU
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"Purification and primary structure of ceratotoxin A and B, two
antibacterial peptides from the female reproductive accessory glands
of the medfly Ceratitis capitata (Insecta:Diptera).";
Insect Biochem. Mol. Biol. 23:591-598(1993)

-1-FUNCTION: FEMALE-SPECIFIC PEPTIDES WITH POTENT ACTIVITY AGAINST
GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. THEY HAVE AS WELL
HEMOLYTIC ACTIVITY. THESE PROTEINS ARE STABLE EVEN AT 100 DEGREES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR;
                                                                                                                                                                                                  Ribosomal protein.
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Halobacteriaceae; Halobacterium.
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SUBUNIT: HOMOPOLYMER OF FOUR TO SIX SUBUNITS.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: STRUCTURALLY RELATED TO CECROPINS, DEFENSINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APIADECINS.
: B61613; B61613.
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9 ALPVAKK 15
                                                                        2 VPIAQKSEPHSLSSEALMRRAV 23
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SE 29 AA; 2861 MW; EE57F4EECB2DA6B0 CRC64;
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Pred. No.
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1: sp_archea:*
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sp_unclassified:*
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                                                               P96173 vibrio sp.
Q2939 oryctolagus
O57546 lampetra pl
Q9jmv3 escherichia
Q8ia94 caenorhabdi
Q8ia94 caenorhabdi
Q8clal yersinia pe
Q9r4w6 helicobacte
O57547 lampetra pl
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720867	Q9x641	Q9x642	Q9x639	Q9s8d9	Q9t2s6	Q8tdj4	Q87579	Q87581	Q87577	Q9x630	Q9wvu7	Q9x634	Q9x632	Q9x629 u	Q9quv8	Q811y8	Q811y7		UI	σ	7		Q9ucr6	Q9gb58	Q9gb43	Q9gb41	09dp60	Q9g1i7
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ALIGNMENTS

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P96173;
01-MAY-1997 (TrEMBLrel. 03, C
01-MAY-1997 (TrEMBLrel. 03, L
01-DEC-2001 (TrEMBLrel. 19, L
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Vibrio sp. (strain 2693).

Bacteria; Proteobacteria; C

Vibrionaceae; Vibrio.

NCBI_TaxID-79682;
Q29399 PRELIMINARY; PRT;
Q29399;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Aspartate carbamoyltransferase from a psychrophilic deep-sea bacterium, Vibrio strain 2693: properties of the enzyme, genetic organization and synthesis in Escherichia coli."; Microbiology 144:1435-1441(1998).

EMBL; Y09786; CAA70922.1; -
SEQUENCE 20 AA; 2241 MW; 35C31F588FBB5D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98274751; PubMed=9611817; Xu Y., Zhang Y., Liang Z.Y., Van de Casteele M., Legrain Glansdorff N.;
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8; Conserv
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Pred. No. 1.9e+02;
3; Mismatches 4
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                                                                                                                                          01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Luciferase alpha-subunit
                   Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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SEQUENCE
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Homeobox protein LpHox4-7A (Fragment)
Lampetra planeri (Brook lamprey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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057546;
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NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98358009; PubMed=9694633;
Sharman A.C., Holland P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Estimation of Hox gene cluster number Int. J. Dev. Biol. 42:617-620(1998). EMBL: AF044802; AAC03006.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Cystic fibrosis transmembrane conductance regulator
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35.0%;
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53.3%;
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. 15, Last sequence it (Fragment).
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                                                                             SEQUENCE FROM N.A.
STRAIN-Bristol N2;
STRAIN-Bristol N2;
Madsen C., Kalicki J., Yoakum
"The sequence of C. elegans cc
"The sequence of Mar-2001) to the El
                   Waterston R.; Submitted (DEC-2002) to the EMBL; AC090999; AA012396.1;
                                                                                                                                                                                                                                                                                       Q8IA94;
01-MAR-2003
01-MAR-2003
01-MAR-2003
 Hypothetical protein SEQUENCE 30 AA; 3:
                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                   STRAIN=Bristol N2;
                                                              SEQUENCE
                                                                                                                                             Science
                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                                                   MEDLINE=99069613;
                                                                                                                                                                                              STRAIN-Bristol
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   Hypothetical protein Y82E9BR.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene.
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Olsson O., Koncz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "LUXAH/Kan-cassette for site-directed bacterial transcription studies."; Submitted (SEP-1999) to the EMBL/GenBa
                                                                                                                                                                           Waterston
                                                                                                                                                                                                                            NCBI_TaxID=6239;
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SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ner A., O'Kane D.J., Szalay A.;
s beta subunit polypeptide of Vibrio harveyi luciferase determines
it emission at 42 degrees C.";
Gen. Genet. 230:385-393(1991).
; AJ249443; CAB96206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00296; bac_luciferase;
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Pro; IPR002103; Bac_luciferase
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41.2%;
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el. 23, Last annotation
Y82E9BR.3b.
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the EMBL/GenBank/DDBJ databases
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                              EMBL/GenBank/DDBJ
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                                                              Matches
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O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
56 kDa major heat shock protein (Fragment).
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                 MEDIINE-95020803; PubMed-7935068; Yokota K., Hirai Y., Haque M., Hayashi S., Isogai H., Nagamachi E., Tsukada Y., Fujii N., Oguma K.; Nagamachi E., Tsukada Y., Fujii N., Oguma K.; "Heat shock protein produced by Helicobacter pylori."; Microbiol. Immunol. 38:403-405(1994).

SEQUENCE 20 AA; 2326 MW; 995EEETC51529BAC CRC64;
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EMBL; AE013778; AAM85323.1;
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STRAIN-KIM5 / Biovar Mediaevalis;
MEDLINE-22137863; PubMed-12142430;
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Bacteria; Proteobacteria;
Enterobacteriaceae; Yersi
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01-MAR-2003
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NCBI_TaxID=210;
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J. Bacteriol. 184:4601-4611(2002).
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4; Mismatche
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Bonk M., Tadros M., Vandekerckhove J., Al-Babili S., Beyer P.; "Purification and characterization of chaperonin 60 and heat-shock protein 70 from chromophasts of Narcissus pseudonarcissus."; plant physiol. 111:931-939(1996).
HSSP; P06139; 1AON.
HSSP; P06139; 1AON.
SEQUENCE 30 AA; 3233 MW; AF5AF69899CF2851 CPCF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9T2P9 PRELIMINARY; PRT; 30 AA.
09T2P9; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Heat Sock protein 60 (Fragment).
Narcissus pseudonarcissus (Daffodil).
Mitochondrion.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Homeobox protein LipHox4-7B (Fragment).
Lampetra planeri (Brook lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=98358009; PubMed=9
Sharman A.C., Holland P.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidac
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Q1-MAR-2003 (TrEMBLrel. 2:
Q1-MAR-2003 (TrEMBLrel. 2:
Q1-MAR-2003 (TrEMBLrel. 2:
ATP-binding cassette subficassette subficassette subfamily C memb
   Q9GB51;
Q9GB51;
01-MAR-2001
01-MAR-2001
01-OCT-2002
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SEQUENCE FROM N.A.

Valor L.M., Campos-Caro A., Carra
Ballesta J.J., Criado M.;

"Transcription Factors NF-Y and
"Transcription Factors NF-Y and
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ATP-binding.
24 AA;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Lamba J.K., Adachi M.,
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01-MAR-2002 (TrEMBLrel.
Neuronal nicotinic recep
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EMBL; AF453877; AAL57840.1;
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J. Biol. Chem. 0:0-0(2
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Mammalia; Eutheria;
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annotation update)
4 subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                       codons.";
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No.
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                                                                                                                                                                                                                                         Db ;
. 2.1e+03;
9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.,
                                                                            27
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                     update)
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update)
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RESULT
Q9GB55
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AC Q9
DT 01
DT 01
DT 01
DT 01
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Best Local S
Matches 8
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Best Local S
Matches 8
            01-MAR-2001
01-MAR-2001
01-OCT-2002
  Cytochrome
                                            Q9GB55;
                                                       Q9GB55
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                           Oxidoreductase; Mitochondrion.
                                                                                                                                                                                                                                InterPro; IPR002429; Cyt_c_ox_2.
Pfam; PF00116; COX2; 1.
                                                                                                                                                                                                                                                   based on mitochondrial sequence data.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
EMBL; AF168441; AAG12284.1;
                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TYEMBLEEL. 16, Created)
01-MAR-2001 (TYEMBLEEL. 16, Last sequence update)
01-CT-2002 (TYEMBLEEL. 22, Last annotation update)
Cytochrome c oxidase subunit II (Fragment).
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                         "Phylogenetic relationships of Micronesian based on mitochondrial sequence data.";
                                                                                                                                                                                                                                                                                               Slikas B.,
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                Archosauria; Aves;
NCBI_TaxID=135984;
                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Slīkas B., Jones I.B., Derrickson S.R., Fleischer R.C. "Phylogenetic relationships of Micronesian white-eyes based on mitochondrial sequence data.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ database EMBL; AF168437; AAG12279.1; -.
InterPro, IPR002429; Cyt_c_ox_2.
Pfam; PF00116; COX2; 1.
OXidoreductase; Mitochondrion.
NON_TER
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NCBI_TaxID=135985;
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Mitochondrion.
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8; Conserv
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l (TrEMBLrel. 16, C)
l (TrEMBLrel. 16, L)
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c oxidase subunit:
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Created)
Last sequence update)
Last annotation updat
t II (Fragment).
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Pred. No.
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                                                                                                                                                                           Score 29;
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ian white-eyes
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RESULT 15
Q9GB45
ID Q9GB4
AC Q9GB4
AC Q9GB4
DT 01-M
DT 01-M
DT 01-M
OT 01-M
OT 01-M
OT 01-M
OT 01-M
OT 01-M
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OX Q9GB4
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Best Local Similarity
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Search completed: October Job time : 33 secs
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Best Local
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Q9GB45;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome c oxidase subunit II (Fragment).
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SILKAS B., Jones I.B., Derrickson S.R., Fleischer R.C.;

Silkas B., Jones I.B., Derrickson S.R., Fleischer R.C.;

Phylogenetic relationships of Micronesian white-eyes (Zosteropidae) based on mitochondrial sequence data.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF168434; AAG12275.1; -.

EMBL; AF168434; AAG12275.1; -.

InterPro; IPR002429; Cyt_c_ox_2.

Pfam; PF00116; COX2; 1.

OXidoreductase; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Slikas B., Jones I.B., Derrickson S.R., Fleischer R.C.;

Phylogenetic relationships of Micronesian white-eyes (Zosteropidae) based on mitochondrial sequence data.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF168443; AAG12287.1; -.

InterPro; IPR002429; Cyt_c_ox_2.

Pfam; PF00116; COX2; 1.

Oxidoreductase; Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zosterops poliogaster poliogaster (Heuglin's white-eye). Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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8; Conserv
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Pred. No. 2.4e+0;
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-359-362-102

US-08-997-362-102

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US-09-95-426-102

US-09-324-542-102

US-09-324-542-102

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US-08-469-260A-254

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US-09-039-642B-2

US-08-746-111-11

US-08-031-538-57

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US-08-433-522A-47

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US-08-031-148-6
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GENERAL INFORMATION:
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                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                APPLICANT: van Grunsven, Wouterus Marinus Johannes WMJ
TITLE OF INVENTION: Diagnostic reagents for the
TITLE OF INVENTION: detection of antibodies to EBV.
                                                      NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                 APPLICANT: Middeldorp, Jaap Michiel JM APPLICANT: van Grunsven, Wouterus Marin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 9.
FILING DATE: 13-MAR-1992
AFTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                           STREET:
                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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               Rockville
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Maryland
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                        1330 Piccard Drive
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1330-A Piccard Drive
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                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                          AKZO NOBEL PHARMA
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/BER: 32,196
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37.5%;
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Best Local
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                                                                                                                                                INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                                FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     FILING DATE: 03-APR-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Middeldorp, Jaap Michiel.
TITLE OF INVENTION: Peptides and nucleic acid sequences
TITLE OF INVENTION: related to the Epstein-Barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION NUMBER: EP 93202659.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy disk
                                                                       STRANDEDNESS:
                                                                                                                                                                NAME: Gormley, Mary E. REGISTRATION NUMBER: 34,409
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/415,838
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/306,078 FILING DATE: 14-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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5. 6008327
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9; Conservative
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Y: USA
Epstein-Barr virus
                                                     ss: single
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Pred. No.
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US-09-354-231B-29
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LENGTH: 30
TYPE: PRT
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CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR FILING DATE: 1997-06-12
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APPLICANT: Shorrosh, Basil S.

TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF FILE REFERENCE: 07148-063002
NAME: Gormley, Mary E.
RECISTRATION NUMBER: 34,409
INFORMATION FOR SEQ ID NO: 6:
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les 9; Conserv
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es 9; Conserv
                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,169
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Middeldorp, Jaap Michiel.
TITLE OF INVENTION: Peptides and nucleic acid sequences related to the Epstein-Barr virus.
                                              ATTORNEY/AGENT INFORMATION: NAME: Gormley, Mary E.
                                                                                                                      FILING DATE: 04-Dec-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                               APPLICATION NUMBER: 08/415,838 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                             CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAHECGHHAFSDYSLLDDVVGLVLHSS 30
                                                                                                                                                                                                                                                                                                                                                                  STREET: 1300 Piccard Drive,
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d Drive, Suite 206
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Pred. No. 86;
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Pred. No. 86;
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ORGANISM: Epstein-Barr virus;
SEQUENCE DESCRIPTION: SEQ ID NO: US-09-205-169-6
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US-08-997-080-102
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; LENGTH: 30
; TYPE: PRT
; ORGANISM: Zea [
                                                                                                                                                                                                                                                                                               Patent No.
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APPLICANT: Fan, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND O:
TITLE OF INVENTION: FATTY ACID CONTENT
FILE REFERENCE: 07148-072001
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: WATSON
APPLICANT: TAN, PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
CURRENT APPLICATION NUMBER: US/NB/007

FILING DATE:
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY NUMBER OF SEQUENCES: 194
                                                                                                                                                                STREET: 2601 E
                                                                                                                             ZIP: 98121
                                                                                                                                                          STATE:
                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                       COUNTRY:
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9; Conserv
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                                                                                                                                                                                   2601 Elliott Avenue,
                                                                                                                                                                                                                                                                   WATSON, JAMES D.
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Pred. No.
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Pred. No. 86;
                                                                                                                                                                                   Suite 4185
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ATTORNEY/AGENT INFORMATION:

11000.1007

APPLICATION NUMBER: CLASSIFICATION:

APPLICATION DATA:

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Patent No.
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Best Local :
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APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347 FILING DATE: August 29, 11996 ATTORNEY, AGENT INFORMATION: NAME: Sleath, Janet REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 11000.1002c2 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sleath, Janet
REGISTON NUMBER: 37,007
REFERENCATION NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                              APPLICATION NUMBER: U FILING DATE: June 12,
                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                APPLICATION NUMBER: US/08/997,362
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2601 Elliott Avenue, Suite 4185
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Visser, Elizabeth
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                                                                                                                               U.S. Patent Application No. 5985287 08/873,970
2, 1997
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US-08-873-970-102
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              Query Match
Best Local :
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                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,970
                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/7
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
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TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: TREATMENT
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                                                                                           TYPE: amino a
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                                                                                                                                                                                                                      REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
                                                                                   TOPOLOGY:
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Similarity 7; Conserv
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Visser, Elizabeth
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Scott, Linda
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46.7%;
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            Score 32;
Pred. No.
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94;
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                         Length 24;
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RESULT 12
US-09-324-542-102
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                                        GENERAL INFORMATION:
                                                          Sequence 102, Application US/09324542 Patent No. 6328978
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                          Query Match
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           APPLICANT: Watson, James D. APPLICANT: Tan, Paul L.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tan, Fau.
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: brastidge, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-DEC-199/
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann
STREET: 2601 Elliott Avenue, 9
                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 200-209-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sleath, Janet REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/095,855
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6160093
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AEEKMEKAVSVARDS 23
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46.7%;
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Treatment and
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Pred. No. 94;
3; Mismatches
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Suite 4185
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                                                                                                                                                                                                                                     Length 24;
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US-08-538-711A-16

; Sequence 16, Application US/08538711A
; Patent No. 5994062
; GENERAL INFORMATION:

APPLICANT:

MULSHINE, JAMES, L.

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                                                                                                                                                                                                         ; NAME/KEY: UNSURE
; LOCATION: (1)...(
US-09-205-426-102
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER APPLICATION NUMBER: 08/705,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 102, Application Patent No. 6406704
                                                                                                                                Matches
                                                                                                                                                                    Query Match
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CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER FILING DATE: 1999-06-02

EARLIER FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.1002c4
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: PRT
ORGANISM: Mycobacterium
                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium vaccae
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NAME/KEY: UNSURE
LOCATION: (1)...
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                                                      AEEKMEKAVSVARDS
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                                                                                                                                Conservative
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46.7%;
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                                                                                                                             Score 32; DB Pred. No. 94; 3; Mismatches
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TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

AN EPITHELIAL PROTEIN AND DNA THEREOF FOR USE IN EARLY CANCER DETECTION

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

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                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,027
FILING DATE: 02-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 75-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: AN EPITHELIAL PROTI
TITLE OF INVENTION: DNA THEREOF FOR USI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                    NERAL INFORMATION:
NERAL INFORMATION:
NELVYN, S.
APPLICANT: MOLSHINE, JAMES, L.
APPLICANT: TOCKMAN, MELVYN, S.
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                   STREET: 345 PARK
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
STRANDEDNESS: Unl
TOPOLOGY: Linear
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                                                                                                                                                                                                 COUNTRY: UZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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Pred. No. 2.1e+02;
4; Mismatches 11
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; LENGTH: 29
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-08-725-027-16
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                                                                                              QΥ
Search completed: October Job time: 17 secs
                                                                                                                     Best Local Similarity 33.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USOB, FILING DATE: 02-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: KATHRYN M. BROWN REGISTRATION NUMBER: 34
                                                                                    2 VPIAQKSEPHSLSSEAL-MRRAVS 24
                                                             6 VDAAMNARPHKVDGRVVEPKRAVS 29
                                                                                                                                                                                                                                                    Unknown
               2, 2003, 09:43:45
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                                                                                                                                                                                                                                                                                                                       16:
                                                                                                                                  4.
                                                                                                                                                 Score 30.5; DB 3; Pred. No. 2.1e+02;
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                                                                                                                                  Mismatches
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length:
    100.0
49.6
49.6
44.7
44.7
44.7
34.8
34.8
34.8
28.2
28.2
28.2
28.2
28.2
29.1
23.8
23.8
23.4
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11:
12:
13:
14:
15:
18:
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                               / Cgn2_6/ptodata/2/pubpaa/US09E_PUBCOME.pep: *
/ Cgn2_6/ptodata/2/pubpaa/US09C_PUBCOME.pep: *
/ Cgn2_6/ptodata/2/pubpaa/US09C_PUBCOME.pep: *
/ Cgn2_6/ptodata/2/pubpaa/US10A_PUBCOME.pep: *
/ Cgn2_6/ptodata/2/pubpaa/US10E_PUBCOME.pep: *
/ Cgn2_6/ptodata/2/pubpaa/US10C_PUBCOME.pep: *
/ Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep: *
/ Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep: *
/ Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep: *
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/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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4 US-10-1068-569-8
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6 US-09-798-116-20
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Sequence 25, Appl
Sequence 25, Appl
Sequence 47499, A
Sequence 80, Appl
Sequence 40008, A
Sequence 6, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 24, Appli
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	Sequence 1534, Ap	1533,	$\boldsymbol{\Phi}$	4	42325,		254,	e 59, Ap	40837,				15203,	Sequence 279, App	14657,	e 1084,	Sequence 40435, A	102,	Sequence 102, App	542,	Sequence 1480, Ap	3695	Sequence 6, Appli	e 29,	29, AF	119,	12,	5, A	Sequence 45, Appl

ALIGNMENTS

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RESULT 2
US-10-068-569-8
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US-09-939-293-7
Sequence 8, Application US/10068569
Publication No. US20020160975A1
GENERAL INFORMATION:
APPLICANT: Srinivasula, Srinivasa M.
APPLICANT: Fernandes-Alpemri, Teresa
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09939293 Patent No. US20020132786A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
TITLE OF INVENTION: AND METHODS OF USING THE SAME
FILE REFERENCE: 480140.465
CURRENT APPLICATION NUMBER: US/09/939,293
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 18
SOFTMARE: FastSEQ for Windows Version 4.0
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Best Local
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Pred. No. 8.5e-15;
; Mismatches 0;
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; NAME/KEY: misc_feature ; LOCATION: (12)..(12) ; OTHER INFORMATION: M is methionine sulfoxide US-09-798-116-20
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US-10-197-634-8
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                                                                                                                                                                                                                                                                                                                                                          Patent No. US20020110 GENERAL INFORMATION:
                                                                                                                                            NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/10197634
Publication No. US20030073629A1
GEMERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
FILE REFERENCE: 480140.479
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Patent No. US20020110851A1
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CURRENT FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity 93.3

Matches 14; Conservative
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Best Local (
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 15
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: AU PQ5995/00 PRIOR FILING DATE: 2000-03-02
                                                                                                                                                                                                                                  APPLICANT: Verhagen, Anne Marie
APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
TITLE OF INVENTION: NO. US20020110851A1e1
FILE REFERENCE: 10338-004US
CURRENT EPPLICATION NUMBER: US/09/798.116
CURRENT FILING DATE: 2001-03-02
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CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
                                                                                   LENGTH: 13
TYPE: PRT
ORGANISM: synthetic
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                          FEATURE:
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93.3%;
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Pred. No. 0.00034;
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Pred. No.
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0.00034;
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; ORGANISM: Homo sapiens
US-09-965-967-18
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US-09-798-116-22
Sequence 22, Application U
; Patent No. US20020110851A1
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                                                                                                                                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 18 LENGTH: 10
                                                                Matches
                                                                                 Query Match
Best Local
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APPLICANT: Shi, Yig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Verhagen, Anne Marie
APPLICANT: Ekert, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0 SEQ ID NO 22 LENGTH: 13
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Best Local :
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/965,967
CURRENT FILLING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,574
PRIOR FILING DATE: 2000-09-29
PRIOR PELICATION NUMBER: 60/256,830
PRIOR PELICATION NUMBER: 60/256,830
PRIOR FILING DATE: 2000-12-20
PRIOR PELICATION NUMBER: 60/256,830
PRIOR FILING DATE: 2000-13-20
PRIOR FILING DATE: 2000-13-20
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                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shi, Yigong
TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
FILE REFERENCE: PU-0031 (01-1739-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU PQ5995/00
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 25
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TITLE OF INVENTION: No. US20020110851A1el Polypeptides, Modulatory Agents Therefor
FILE REFERENCE: 10338-004US
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AVPIAQKSEP
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ilarity 100.0%;
Conservative
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100.0%; Pr
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100.0%;
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RESULT

US-09-965-967-25

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APPLICANT: Shi, Yigong

TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis

FILE REFERENCE: PU-0031 (01-1739-1)

CURRENT APPLICATION NUMBER: US/09/965,967

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: 60/236,574
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SOFTWARE: Patentin version 3.0
SEQ ID NO 25
LENGTH: 29
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                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                       Sequence 47499, Application US/09864761 Patent No. US20020048763A1
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Best Local Similarity
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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PRIOR APPLICATION NUMBER: AU PQ5995/00
PRIOR FILING DATE: 2000-03-02
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APPLICANT: Vaux, David
TITLE OF INVENTION: No. US20020110851A1el Polypeptides, Modulatory Agents Therefor an
FILE REFERENCE: 10338-004US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Verhagen, Anne Marie
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100.0%; Pred. No.
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Pred. No.
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Best Local
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                                                                                      APPLICANT: Min, Hosung
APPLICANT: Sitney, Karen
APPLICANT: Hartley, Cynthia
TITLE OF INVENTION: Peptides and Related Compounds Having Thrombopoietic Activity
FILE REFERENCE: A-750
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
CURRENT APPLICATION NUMBER: US/10/269,806
CURRENT FILING DATE: 2002-10-10
NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO AC022267.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL -
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL -
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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8; Conserv
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Pred. No. 76;
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                                                            SEQ ID NO 40008
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                                                                              PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engi
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                     LENGTH: 29
TYPE: PRT
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ORGANISM: Homo sapiens
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LENGTH: 25
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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FILING DATE: 2001-01-30
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Chen, Wensheng
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NIMBER: US 09/632,366
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2.2e+02;
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; ORGANISM: HO
US-09-965-967-8
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US-09-965-967-8
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US-09-939-293-6
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                                                                                                            SOFTWARE: 1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 7
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APPLICANT: Shi, Yig
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 Query Match
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Best Local
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PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/256,830
PRIOR FILING DATE: 2000-12-20
                                                                                                                                                                                                                                         APPLICANT: Shi, Yigong
TITLE OF INVENTION: Compositions and Methods For Regulating Apoptosis
FILE REFERENCE: PU_0031 (01-1739-1)
CURRENT APPLICATION NUMBER: US/09/965,967
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE TITLE OF INVENTION: AND METHODS OF USING THE SAME FILE REFERENCE: 480140.465

CURRENT APPLICATION NUMBER: US/09/939,293

CURRENT FILING DATE: 2001-08-24
                                                                                                                                                   NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
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R INFORMATION:
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                                                          Homo
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NN: EXPRESSED IN LUNG, SIGNAL = 8

NN: EXPRESSED IN PLACENTA, SIGNAL = 7.2

NN: EXPRESSED IN HEART, SIGNAL = 7.4

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 7.8

NN: EXPRESSED IN BRAIN, SIGNAL = 7.8

NN: EXPRESSED IN BONE MARROW, SIGNAL = 7.5

NN: EXPRESSED IN HELA, SIGNAL = 8.2

NN: EXPRESSED IN HELA, SIGNAL = 8.2

NN: EXPRESSED IN HELA, SIGNAL = 8.2

NN: EXPRESSED IN HELA, SIGNAL = 8.6

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 8.6

NN: EXPRESSED IN BONE MARROW, SIGNAL = 8.6
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23.4%;
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 Score 33;
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Pred. No. 3.1e+02;
2; Mismatches 7;
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 10;
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 Length 7;
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CURRENT APPLICATION NUMBER: US/10/293,371
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US 60/370,934
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/332,300
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEO ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
7; Conserve
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; OTHER INFORMATION: Synthetic
US-10-293-371-1
; TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER IMPORMATION: Synthetic
US-10-293-371-24
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                                                                                                                NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/10293371 Publication No. US20030157522A1
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                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/293,371 CURRENT FILING DATE: 2003-04-08 PRIOR APPLICATION NUMBER: US 60/370,934 PRIOR FILING DATE: 2002-04-08 PRIOR APPLICATION NUMBER: US 60/332,300 PRIOR APPLICATION NUMBER: US 60/332,300 PRIOR FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                         APPLICANT: BOUDREAULT, ALAIN
APPLICANT: KORNELUK, ROBERT G.
APPLICANT: LACASSE, ERIC
APPLICANT: LISTON, PETER
TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
TITLE OF INVENTION: Interaction Screens
FILE REFERENCE: 07891/030002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BOUDREAULT, ALAIN
APPLICANT: KORNELUK, ROBERT G.
APPLICANT: LACASSE, ERIC
APPLICANT: LACASSE, ERIC
TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
TITLE OF INVENTION: Interaction Screens
TILE REFERENCE: 07891/030002
                                                                                                   ENGTH:
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Pred. No. 5.2e+05;
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Query Match 23.4%; Score 33; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 AVPIAQK 7
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Db 1 AVPIAQK 7
Search completed: October 2, 2003, 09:44:16
Job time: 23 secs
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; SEQ ID NO 8; LENGTH: 177; TYPE: PRT; ORGANISM: Homo sapiens US-09-798-116-8
                                                                      ; SOFTWARE: PatentIn version 3.0; SEQ ID NO 6; LENGTH: 177; TYPE: PRT; ORGANISM: Mus musculus US-09-798-116-6
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US-09-798-116-9
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   Best Local
Matches 2
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Best Local Similarity
Matches 23; Conserv
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APPLICANT: Vaux, David
TITLE OF INVENTION: No. US20020110851Alel Polypeptides, Modulatory Agents Therefor an FILE REFERENCE: 10338-004US
CURRENT APPLICATION NUMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU pc5995/00
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Verhagen, Anne Marie APPLICANT: Ekert, Paul
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APPLICANT: Vaux, David
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SOFTWARE: PatentIn version 3.0
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                  74.58;
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90.0%;
Score 105; DB 10;
Pred. No. 2.5e-08;
1; Mismatches 0;
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Pred. No. 8.4e-12;
2; Mismatches 1;
                                 Length 177;
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; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-197-634-8
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Search completed: October Job time: 24 secs
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US-10-068-569-8
                                                                                                                                              Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 480140.479
CURRENT APPLICATION NUMBER: US/10/197,634
CURRENT FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
TITLE OF INVENTION: IAP-CASPASE INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
NUMBER OF SEO ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
FILE REFERENCE: 480140.475
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alnemri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Srinivasula, Srinivasa M.
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TYPE: PRT
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93.3%;
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Pred. No.
                                                                                                                                              Score 70; DB 15;
Pred. No. 0.00034;
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RESULT 9
US-09-798-116-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-10-141-618-14
Sequence 2, Application US/09798116
                                                                                                                                                                                                                                                                                                     SEQ ID NO 348
LENGTH: 239
                                                                                                                                                                                                         Query Match
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Best Local
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APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/289,233
PRIOR EILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 60/356,934
PRIOR EILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: US 09/388,221
PRIOR FILING DATE: 1999-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/153,668 CURRENT FILING DATE: 2002-05-24
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APPLICANT: MATSU
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 488
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 2001-313175 PRIOR FILING DATE: 2001-10-10
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CURRENT APPLICATION NUMBER: US/10/141,618
CURRENT FILING DATE: 2002-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Methods For Determining the Prognosis TITLE OF INVENTION: For Cancer Patients Using Tucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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les 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 2001-157043
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                                                                                           AVPIAQKSEPHSLSSEALMRRAVSLVTDST 85
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Pred. No. 9.8e-14;
; Mismatches 0;
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Pred. No. 9.8e-14;
Mismatches 0;
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RESULT 11
US-09-798-116-9
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APPLICANT: Verhagen, Anne Marie
APPLICANT: Ekert, Paul
APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
TITLE OF INVENTION: No. US20020110851A1el Polypeptides, Modulatory Agents Therefor
FILE REFERENCE: 10338-004US
CURRENT APPLICATION NUMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU PQ5995/00
PRIOR FILING DATE: 2000-03-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NO. US20020110851A1e1 FILE REFERENCE: 10338-004US CURRENT APPLICATION NUMBER: US/09/798,116 CURRENT FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Verhagen, Anne Marie
APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
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CURRENT FILING DATE: 2001-03-02
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TYPE: PRT
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29; Conserv
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29; Conservative
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Vaux, David
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96.78;
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Pred. No. 2.8e-13;
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1; Mismatches
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Pred. No. 2.8e-13;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-293-8
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; ORGANISM: Homo sapiens
US-09-939-293-11
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GENERAL INFORMATION:
APPLICANT: Allemri, Emad S.
APPLICANT: Allemri, AN IAP PEPTIDE OR POLYPEPTIDE
TITLE OF INVENTION: AND METHODS OF USING THE SAMI
FILE REFERENCE: 480140.465
CURRENT APPLICATION NUMBER: US/09/939,293
CURRENT FILING DAATE: 2001-08-24
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; SOFTWARE: FastSEQ f
; SEQ ID NO 11
; LENGTH: 35
                                                                          Query Match
Best Local
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Patent No. US20020132786A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/939,293
CURRENT FILING DATE: 2001-08-24
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TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
TITLE OF INVENTION: AND METHODS OF USING THE SAMI
                                                                                                                                                     TYPE: PRT
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AVPIAQKSEPHSLSSEALMRRAVSLVTDST
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                                                     Score 141; DB 10;
Pred. No. 1.2e-14;
; Mismatches 0;
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Pred. No. 1.2e-14;
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Pred. No. 1e-14;
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RESULT 7
US-10-141-618-14
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                                                                                                                                                                                                                       US-09-925-297-591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-925-297-591; Sequence 591, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-09-798-116-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-798-116-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 591, Application US/09925297 Patent No. US20020081659A1 CEMERAL INFORMATION:
                                                                                                                                               Best Local Similarity Matches 30; Conserv
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 591
LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 7
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Best Local Similarity
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Patent No. US20020110851A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NO. US20020110851A1el Polypeptides, Modulatory Agents Therefor FILE REFERENCE: 10338-004US
CURRENT APPLICATION NUMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU P05995/00
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Verhagen, Anne Marie
APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 928
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 20
TYPE: PRT
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                                                                                                                                                                                                                                      NAME/KEY: SITE LOCATION: (1) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                           ORGANISM: HOMO FEATURE:
                                                                         44
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                                                                                          1 AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30
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                                                                                                                                                            Score 141; DB 9;
Pred. No. 9.2e-14;
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Sequence 14, Application US/10141618 Publication No. US20030165887A1 GENERAL INFORMATION:

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Result
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Maximum DB
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Maximum Match 100%
Listing first 45 summaries
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:/cgn2_6/ptodata/2/pubpaa/USO9B_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
:/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
:/cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/USIOC_NEW_PUB.pep:*
:/cgn2_6/ptodata/2/pubpaa/USIOC_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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10 US-09-939-293-11
10 US-09-939-293-8
10 US-09-939-293-8
10 US-09-939-116-7
10 US-09-925-297-91
11 US-10-141-618-14
15 US-10-153-668-348
16 US-09-798-116-9
10 US-09-798-116-9
10 US-09-798-116-8
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Sequence 7, Appli
Sequence 11, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 591, App
Sequence 14, Appli
Sequence 348, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 8, Appli
                                                                                                                                                                                                                                                                Description
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US-09-939-293-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Alnemati, Emad S.
APPLICANT: Alnemati, Emad S.
TITLE OF INVENTION: AN IAP PEPTIDE OF POLYPEPTIDE
TITLE OF INVENTION: AND METHODS OF USING THE SAME
FILE REFERENCE: 480140.465
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09939293 Patent No. US20020132786A1
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/939,293
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 18 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                               LENGTH: 30
TYPE: PRT
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ALIGNMENTS

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RESULT 2
US-09-939-293-11
; Sequence 11, Application US/09939293
; Patent NO. US20020132786A1
; GENERAL INFORMATION:
    APPLICANT: Alnemri, Emad S.
    TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
; TITLE OF INVENTION: AND METHODS OF USING THE SAME
; FILE REFERENCE: 480140.465
; CURRENT APPLICATION NUMBER: US/09/939,293
                                                                                                                                                                                                                                                         1 AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 8.5e-15;
); Mismatches 0;
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RESULT 8
ABB76228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI (DIABLO), but with the native N-terminal alanine residue (see ABB76209) acetylated. Claimed smac-derived peptides (see ABB76209) bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Modification of the N-terminal alanine destroys all binding affinity for the protein. Thus, Kd values for Bir-3 and Bir-2 were each over 1,000 uM for the present peptide, compared with 0.43 +/- 0.06 uM and 6.0 +/- 0.9 uM, respectively, for the corresponding wild-type peptide. The claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to
                                                                                                                                human;
                                                                                                                                              DIABLO;
                                                                                                                                                                         Fluorosceinated
                                                                                                                                                                                                  09-AUG-2002
                                                                                                                                                                                                                                                     ABB76228 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIVOLIVES DETERMINATION OF THE ability of candidate compounds to disrupt the binding interaction between a smac peptide and an IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                           Synthetic.
                                                                                                                                                                                                                            ABB76228;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-2000; 2000US-0687549
                WO200230959-A2
                                                     Modified-site
                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a peptide derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fesik SW,
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                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                  cancer;
                                                                                                                                               smac;
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                 (first entry)
                                                                                                                               inhibitor of apoptosis protein; IAP; apoptosis;
; cytostatic; mutant; mutein.
                                                                                                                                                                        smac
                                                                 Location/Qualifiers
                                         /note-
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                                                                                                                                                                       (DIABLO)
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                                         "N-terminal fluorescein"
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Pred. No.
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                                                                                                                                                                       derived peptide
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9.3e+05;
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ABG72319
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Best Local :
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WPI; 2003-074681/07
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                        Verhagen AM,
                                                                                                                                                          US2002110851-A1.
                                                                                                                                15-AUG-2002.
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                              liver
                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                    29-JAN-2003
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                                                                                                                                                                                                             disease;
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fluorescence polarisation-based competition assay designed to determine the binding affinity of variant smac peptides (see ABB76206-27) to the Bir-3 and Bir-2 domains of XIAP, an inhibitor of apoptosis protein (IAP) family member. Claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                                                                                                    Human; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP: cancer; vascular disease; hepati autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence corresponds to amino acids 1-9 of human second mitochondria derived activator of caspase (smac), also as direct inhibitor of dapptosis binding protein with low pI (DIABLO), but is fluorosceinated. The peptide was used in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells - \,
                                                                                                       02-MAR-2000; 2000AU-0005995
                                                                                                                                                            02-MAR-2001; 2001US-0798116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pro-apoptotic protein DIABLO peptide sequence
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AA;
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Ekert PG,
                                                     INST MEDICAL RES WALTER &
                                                                                                                                                                                                                                                                                                                                                                              immunogen.
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Pred. No.
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ABG24798
ID ABG24
XX ABG24
AC ABG24
XX 18-FE
DT 18-FE
XX Human
KW food
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CC expression vectors, transformed host cells, producing a biologically constitute fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP) cof the IAP), producing a natural or synthetic variant of DIABLO (cof the IAP), producing a natural or synthetic variant of DIABLO (cof the IAP), producing a natural or synthetic variant of DIABLO (cof the IAP), producing a natural or synthetic variant of DIABLO (cof the IAP), producing a natural or synthetic variant of DIABLO (cof binding molecule that specifically binds to DIABLO or its fragment, cof detecting DIABLO in a biological sample (by contacting the sample (cof with an IAP and detecting the presence of an IAP/DIABLO complex), comparison and composition for treatment/prophylaxis of a DIABLO, is conducting the death of a cell (by contacting a cell with an composition for treatment/prophylaxis of a DIABLO, is conduction comprising an agent which reduces the level/activity of a coplypeptide or DIABLO, or a nucleic acid encoding DIABLO, is considered to the modulates the level and/or functional activity of a polypeptide comprising mature or pro-human DIABLO in a biological sample. The agent which modulates the level and/or functional activity of a polypeptide comprising mature or pro-human DIABLO polypeptide, is cuseful for the treatment and/or prophylaxis of a condition associated with services of a sasociated with heart condition activity of a cassociated with cell death or apoptosis. The present sequence comprising protein sequence from human DIABLO, which co-precipitates with the human IAP protein MIHA (not defined).
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Best Local Similarity
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                           31-MAR-2000;
23-AUG-2000;
                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                          WO200175067-A2
                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #24789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG24798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell death or apoptosis e.g. cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 AVSLVTDST
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                           2000US-0540217
2000US-0649167
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biologically active fragment of 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        score 40; DB; Pred. No. 21; 0; Mismatches
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21;
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RESULT 11
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                               Modified-site
                                                                                                                                Misc-difference
                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                 Homo sapiens:
                                                                                                                                                                                                                                              DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                                                                                 Human smac (DIABLO) derived
                                                                                                                                                                                                                                                                                                                    09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                     ABB76218;
                                                                                                                                                                                                                                                                                                                                                                                      ABB76218 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques
                                                WO200230959-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                  human; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 55157; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated
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                                                                                                                                                                                                                                cytostatic; mutant; mutein.
                                                                                                                                  Location/Qualifiers
                                                                                /note=
                                                                                                               /note= "wild-type Ala substituted by Phe"
                                                                                                                                                                                                                                                                                                                                                                                      Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.7%;
26.1%;
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                                                                              "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                 peptide
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Pred. No.
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32;
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Novel Smac peptides and polynucleotides for stimulating apoptosis in neoplastic overexpresses inhibitor of caspase, and

encoding the peptides, useful or tumour cell which for identifying apoptosis

compounds

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC and an isolated nucleic acid (II) encoding (I). Also described is a CC method of identifying a compound that inhibits apoptosis, comprising: CC (a) separately contacting several cell populations expressing a CC cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, (I)). CC and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting) CC domain) with a compound to be tested for apoptotic inhibiting activity; (b) incubating the cell populations with a direct stimulus of the cell cell populations with a direct stimulus of the cell cell populations, where inhibition of the specific apoptotic activity is CC indicative that the compound is an inhibitor of apoptotic activity is CC indicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac polypeptide and CC polynucleotide are useful for stimulating apoptosis. (I) and (II) CC are useful for identifying apoptosis in a neophastic or CC inhibitor inhibits activation or activity of caspase, where the CC inhibitor inhibits activation or activity of caspase, where the CC inhibitor inhibits are presented or activity of caspase and poptosis which involves contacting a cell transformed or CC inhibitor inhibitor inhibitor or activity of caspase. (I) and (II) is useful for identifying an inhibitor or enhancer of a caspase in CC cell viability indicates the presence of an inhibitor and adecrease in CC cell viability indicates the presence of an inhibitor and adecrease in cell viability indicates the presence of an inhibitor and an increase in processing indicates the presence of an enhancer. Optionally, the compound that inhibits small submits of CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for CC caspase-1, caspase-1 or caspase-9 are detected. (I) is also useful for CC caspase-1, cas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local (
                                                        Rat; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepatic disease; autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
  Rattus
                                                                                                                                                               Rat partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                       29-JAN-2003
                                                                                                                                                                                                                                                                                     ABG72303 standard; Protein;
                                                                                                                                                                                                                                               ABG72303
                                         liver
                                         disease;
qs
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7; Conserv
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                                                                                                                                                               for
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                                                                                                                                                           pro-apoptotic protein DIABLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33;
Pred. No.
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Gaps

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with an IAP and detecting the presence of an IAP/DIABLO complex), modulating the death of a cell (by contacting a cell with an agent, which modulates the level and/or functional activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO relate condition comprising an agent which reduces the level/activity of a polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is useful for screening for an agent which modulates cell death. An antigen-binding molecule is useful for detecting DIABLO in a biological sample. The agent which modulates the level and/or functional activity of a polypeptide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with expression or activation of DIABLO, such as cancer, vascular disease, hepatic disease, autoimmune disease and neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                designated DIABLO, or its biologically active fragment of 8 amino aci in length. Also included are the polynucleotide encoding DIABLO, expression vectors, transformed host cells, producing a biologically active fragment of DIABLO (by contacting an inhibitor of apoptosis (I with a fragment of the polypeptide, and detecting a reduction in acti of the IAP), producing a natural or synthetic variant of DIABLO with cell death activity or which reduces IAP activity, an antigenbinding molecule that specifically binds to DIABLO or its fragment, detecting DIABLO in a biological sample (by contacting the sample detecting DIABLO) in a biological sample (by contacting the sample)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell death or apoptosis \mathbf{e}_i g . cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2000; 2000AU-0005995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002110851-A1
                                                                associated with cell death or apoptosis. The
                                                                                     DIABLO is also useful for treatment and/or prophylaxis of conditions
                                                                                                                                  disease, tissue damage or muscular tissue damage associated with heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 35; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-074681/07
                                                                                                          or hepatic_tissue damage associated with
                                          partial rat DIABLO
84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INST MEDICAL RES
ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to an isolated pro-apoptotic polypeptide, its biologically active fragment of 8 amino acids
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                                                                    present sequence
                                                                                                                  a liver
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(IAP)

of.

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Matches
                                 Query Match
Best Local
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4
            1 AVPIAQK 7
                          7; Conserv
AVPIAQK 60
                           Conservative
                                 100.0%;
                                 Score 33;
Pred. No.
                           Mismatches
                                   N
                                  DB 24;
2.9;
                           0;
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Length 84

0

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RESULT 15
ABG72302
                                                      ABG72302 standard; Protein;
29-JAN-2003
                            ABG72302
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Human partial sequence for pro-apoptotic protein DIABLO

(first entry)

autoimmune disease; Human; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepat neurodegenerative disease; tissue damage; hepatic disease;

(OTARU) XNALE BLANK (USPTO)

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Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                         Match
100.0
68.1
49.6
44.7
44.7
29.8
29.8
29.8
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2: \SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *
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14: \SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT: *
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                    AAU78435
ABB76208
ABP71314
ABG72314
ABG72316
ABB76209
ABB76229
ABB76228
                                                                                                                                                                                                                                                                                                                     SUMMARIES
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                                                                                                                                                                                                                                           Description
                                                                                            Human
Human
                                           Human smac
                                                                       Human
                                                                                                                                               Human
                                                                                                                                                                 Inhibitor of apopt
Human smac (DIABLO
                       Fluorosceinated sm
                                      pro-apoptoti
pro-apoptoti
smac (DIABLO
smac (DIABLO
                                                                                                                                          Smac protein
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						-				7 23																							9 23		30 22
ABB36299	ABB76219	AAY95833	AAW99319	AAR74988	AAR42319	AAM83269	AAY45327	AAU78487	AAU78434	ABB76213	AAU85044	ABG43702	AAM33999	AAM20109	AAM73813	AAM61105	ABB24710	ABB40307	ABG55563	AAW25067	ABB76223	ABB76216	ABB76211	ABB76210	ABB44274	ABG59643	ABB76224	ABB76212	ABB76227	ABB76226	ABB76225	ABB76222	ABB76221	ABB76218	ABG24798
	•																		-																
Peptide #3805 enco	Human smac (DIABLO	Native human LAMP-	Epstein-Barr virus	Epstein-Barr virus	EBV VCA peptide.	Human immune/haema	Human secreted pro	Smac-7 AV peptoid.	Inhibitor of apopt	Human smac (DIABLO	MAGE-3 s	Human peptide enco	Peptide #8036 enco		Human bone marrow	brain e	#6709	Peptide #7813 enco	iver p	cancer	Human smac (DIABLO	Human smac (DIABLO	smac	Human smac (DIABLO	Peptide #11780 enc	Human liver peptid	Human smac (DIABLO	smac (smac (smac (Human smac (DIABLO	Human smac (DIABLO	smac	_	Novel human diagno

ALIGNMENTS

RESULT 1 AAU78435 18-JUN-2002 (first entry) AAU78435; AAU78435 standard; Peptide; Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N30. 30

Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2; Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy; neoplastic cell; mutant; tumour.

Homo sapiens

Synthetic.

28-FEB-2002. WO200216418-A2

24-AUG-2001; 2001WO-US26492

(UYJE-) UNIV JEFFERSON THOMAS 24-AUG-2000; 2000US-227735P.

WPI; 2002-304115/34

Novel Smac peptides and polynucleotides encoding the peptides, useful

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RESULT 2
ABB76208
ID ABB7
XX ABB7
AC ABB7
XX U9-A
XX Huma
DE Huma
XX DIAB
KW DIAB
KW DIAB
KW huma
XX Homc
XX Homc
XX Homc
XX Homc
XX Wodi
FT Modi
XX WO20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated Smac peptide or polypeptide (I) CC and an isolated nucleic acid (II) encoding (I). Also described is a CC method of identifying a compound that inhibits apoptosis, comprising: CC (a) separately contacting several cell populations expressing a CC vytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting CC domain) with a compound to be tested for apoptotic inhibiting activity; (b) incubating the cell populations with a direct stimulus of the cell cell populations, where inhibition of the specific apoptotic activity is confidently that the compound is an inhibitor of apoptosis. (I) and (II) (CC call populations, where inhibition of the specific apoptotic activity is confidently that the compound is an inhibitor of apoptosis. (I) and (II) (CC caspase-9) are useful for stimulating apoptosis in a neophastic or tumour cell which overexpresses an inhibitor of caspase, where the CC inhibitor inhibits activation or activity of caspase-3, caspase-7 or created apoptosis which involves contacting a cell transformed or transfected with a vector expressing (I) with a candidate inhibitor or enhancer of a caspase-1 (CC call viability indicates the presence of an inhibitor and a decrease in method involves detecting the presence of an inhibitor and a decrease in cell viability indicates the presence of an enhancer. Optionally, the cell presence of an inhibitor and a decrease in processing indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an inhibitor and a decrease in the processing indicates the presence of an inhibitor of an inhibitor of caspase-3, caspase-7 or caspase-9, caspase-7 or caspase-9, caspase-1, caspase-9 are detected. (I) is also useful for caspase-9, caspase-1 or caspase-9 are detected. (I) is also useful for caspase-1 or fare the cell of the caspase in the processing indicates 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                   WO200230959-A2
                                                                           Modified-site
                                                                                                                                      Homo
                                                                                                                                                                          human;
                                                                                                                                                                                                                               Human smac (DIABLO) derived
                                                                                                                                                                                                                                                                       09-AUG-2002
                                                                                                                                                                                                                                                                                                              ABB76208
                                                                                                                                                                                                                                                                                                                                            ABB76208 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for stimulating apoptosis in neoplastic overexpresses inhibitor of caspase, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modulating compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                  sapiens
                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
30; Conser
                                                                                                                                                                                           smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Fig 7; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                       AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                        inhibitor of cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÀΑ;
                                                                           Location/Qualifiers 20
                                                     "optional C-terminal protecting group
                                                                                                                                                                                       apoptosis protein;
                                                                                                                                                                                                                           peptide.
                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141; DB 23;
Pred. No. 2.2e-16;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or tumour cell which for identifying apoptosis
                                                                                                                                                                                     IAP; apoptosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 3
ABP71314
ID XXX ACC CONTROL OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of XIAP, an inhibitor of apoptosis protein (IAP) family member. Rd values for Bir 3 and Bir 2 are 0.69 +/- 0.05 uM and 6.7 +/- 0.7 uM, respectively, for the present peptide, compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively, for full-length smac. Modification of the N-terminal alanine destroys binding affinity to XIAP. For example, N-terminal alanine with glycine, propionic acid or isobityric acid all resulted in Kd values for Bir 3 and for Bir 2 of over 1.000 uM. The claimed peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac (DIABLO) peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                                                                  Omi; HtrA2; serine protease; inhibitor of apoptosis protein; IAP; caspase; apoptosis; cytostatic; immunosuppressive; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP71314 standard; peptide;
                       13-JUL-2001;
14-DEC-2001;
                                                                                                          15-JUL-2002;
                                                                                                                                                                     23-JAN-2003
                                                                                                                                                                                                                             WO2003006680-A2
                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                           vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP71314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a peptide derived from wild-type human second mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived peptides (see ABB76208-19) which bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substances
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fesik SW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVPIAQKSEPHSLSSEALMR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVPIAQKSEPHSLSSEALMR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 7; 26pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meadows RP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                       2001US-305378P.
2001US-340163P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                             2002WO-US22658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US32121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>1</u>5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
4.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olejniczak ET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides encoding an Omi (serine protease) peptide or polypeptide. The Omi peptide specifically binds to a portion of an Inhibiting Apoptosis Protein (IAP). The Omi polypeptide induces caspase-independent apoptosis, or fails to have serine protease activity. The Omi peptides are useful for regulating or altering apoptosis, specifically caspase-mediated apoptosis, and as immunogens for raising antibodies. Enhancers of apoptosis are useful for treating cancers, tumours or for destroying cells that mediate autoimmune diseases. Compositions may also be used for the treatment of diseases associated with inappropriate activation of apoptosis such as neurodegenerative diseases and ischaemic injury. The antibodies can be used in isolating omi peptides, polypeptides and their variants, in clean in the stream of the peptides and polypeptides and in inhibiting or enhancing the biological activity of omi peptides and polypeptides. Sequences ABP71310-315 represent fragments of various captured to the period of the period of the period of the control of the control of the period of the control of the period of the control of the period of the control of the control of the period of the control of
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                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepatic disease; autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Omi nucleic acids and peptides that bind apoptosis proteins, useful for regulating or apoptosis and for treating cancer, tumor, or
                                                                                                                                                                                                         US2002110851-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG72314 standard; Peptide; 13
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                       (HALL-) HALL INST MEDICAL RES WALTER & ELIZA
                                                                    02-MAR-2000; 2000AU-0005995
                                                                                                            02-MAR-2001; 2001US-0798116
                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAP-binding proteins, used to determine Omi as a IAP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYJE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pro-apoptotic protein DIABLO peptide sequence #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVPIAQKSEPHSLSN 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                           immunogen
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                         /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.6%;
                                                                                                                                                                                                                                                 "Methione is methionine sulphoxide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor, or autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24; I
7.7e-05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to an inhibitor of altering caspase-mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 5
ABG72316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC with an IAP and detecting the presence of an IAP/DIABLO complex),

CC modulating the death of a cell (by contacting a cell with an

CC agent, which modulates the level and/or functional activity of a

CC polypeptide, a composition for treatment/prophylaxis of a DIABLO related

CC polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is

CC useful for screening for an agent which modulates cell death. An

CC antigen-binding molecule is useful for detecting DIABLO in a biological

CC sample. The agent which modulates the level and/or functional activity of

CC apolypeptide comprising mature or pro-human DIABLO polypeptide, is

CC useful for the treatment and/or prophylaxis of a condition associated

CC useful for the treatment and/or prophylaxis of a condition associated

CC with expression or activation of DIABLO, such as cancer, vascular

CC disease, hepatic disease, autoimmune disease and neurodegenerative

CC disease, tissue damage or muscular tissue damage associated with heart

CC attack, or hepatic tissue damage associated with a liver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence represents a partial peptide sequence from human DIABLO, identified by protein sequencing of a protein (later identified as DIABLO) which co-precipitates with the human IAP protein MIHA (not defined).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in length. Also included are the polynucleotide encoding DIABIO, expression vectors, transformed host cells, producing a biologically active fragment of DIABIO (by contacting an inhibitor of apoptosis () with a fragment of the polypeptide, and detecting a reduction in activith (and the IAP), producing a natural or synthetic variant of DIABIO with cell death activity or which reduces IAP activity, an antigenbinding molecule that specifically binds to DIABIO or its fragment, detecting DIABIO in a biological sample (by contacting the sample
                                                                                                                                      Human; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepati autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                  ABG72316 standard; Peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino acids
                                                                                                                                                                                                                                                                                   29-JAN-2003
                                                                                                                                                                                                                                                                                                                            ABG72316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          designated
in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Page 4; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             death or apoptosis e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell
                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Verhagen
                                                                                                                       liver
                                                                                                                     disease;
                                                                                                                                                                                                                                           pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEPHSLSSEALMR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEPHSLSSEALMR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                   immunogen
                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaux DL;
                                                                                                                                                                                                                                             DIABLO peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
0.00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 13
                                                                                                                                                                                                                                             #12.
                                                                                                                                                                                 hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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US2002110851-A1

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RESULT 6
ABB76209
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CC in length. Also included are the polynucleotide encoding DIABLO.

CC expression vectors, transformed host cells, producing a biologically

CC active fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP)

CC with a fragment of the polypeptide, and detecting a reduction in activity

CC with cell death activity or which reduces IAP activity, an antigen-

CC binding molecule that specifically binds to DIABLO or its fragment,

CC with an IAP and detecting the presence of an IAP/DIABLO complex),

CC modulating the death of a cell (by contacting a cell with an

CC engent, which modulates the level and/or functional activity of a

CC condition comprising an agent which reduces the level/activity of a

CC useful for screening for an agent which modulates cell death. An

CC useful for screening for an agent which modulates cell death. An

CC sample. The agent which modulates the level and/or functional activity of a

CC useful for the treatment and/or prophylaxis of a DIABLO, is

CC useful for the treatment and/or prophylaxis of a condition associated

CC with expression or activation of DIABLO, such as cancer, vascular

CC disease, hepatic disease, autoimmune disease and neurodegenerative

CC disease, tissue damage or muscular tissue damage associated with heart

CC associated with cell death or apoptosis. The present sequence

CC represents a partial peptide sequence from human DIABLO, which

CC operations expending of a protein (later identified as DIABLO) which

CC operations of a partial peptide sequence from human DIABLO, which

CC operations are with the human IAP protein MIHA (not defined).
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                Matches
Homo sapiens
                                              DIABLO;
                                                                                  Human smac (DIABLO) derived peptide
                                                                                                                     09-AUG-2002
                                                                                                                                                         ABB76209
                                                                                                                                                                                     ABB76209 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated pro-apoptotic polypeptide, designated DIABEO, or its biologically active fragment of 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             death or apoptosis e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HALL-) HALL INST MEDICAL RES WALTER & ELIZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pro-apoptotic polypeptide, useful for screening for agents which late cell death and for treating conditions associated with cell
                                 cancer;
                                                                                                                                                                                                                                                                                                                                               l Similarity
13; Conser
                                                smac;
                                                                                                                                                                                                                                                                             SEPHSLSSEALMR 13
                                                                                                                                                                                                                                                                                                           SEPHSLSSEALMR 20
                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 4; 50pp;
                                                                                                                                                                                                                                                                                                                                             ilarity 100.0%;
Conservative (
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000AU-0005995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0798116
                                          inhibitor of apoptosis protein; IAP; apoptosis;
                                cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PG,
                                                                                                                                                                                                                                                                                                                                                                               44.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaux DL
                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                           Score 63;
Pred. No.
                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                           DB 24; 1
                                                                                                                                                                                                                                                                                                                                                                           Length 13
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 7
ABB76229
ID ABB7
Дb
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               second mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived paptides (see ABB76208-19) which bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Kd values for Bir-3 and Bir-2 are 0.43 +/- 0.06 uM and 6.0 +/- 0.9 uM, respectively, for the present peptide, compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively, for full-length smac. Modification of the N-terminal alanine destroys binding affinity to XIAP, and mutation of the valine, proline or isoleucine also causes some loss of binding. Amino acids C-terminal to the isoleucine are not important for binding. The claimed peptides can be used to identify candidate substances which induce or promote apoptosis in cells who aceasy involves determination of the absolution of the paper involves determination of the apoptosis in a shifty of the aceasy involves determination of the absolution are shifty of the aceasy involves determination of the absolution are shifty of the aceasy involves determination of the ability of the aceasy involves determination of the shifty of the aceasy involves determination of the aceasy involv
                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                    DIABLO;
                                                                                                                                                                                                                                                                                                                                                             Human smac (DIABLO) derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB76229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB76229 standard; Peptide;
                                  Misc-difference
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                          human;
                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between smac (DIABLO) peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a peptide derived from wild-type human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-2000; 2000US-0687549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2001; 2001WO-US32121
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                        smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVPIAQKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 7; 26pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.8%; Silarity 100.0%; Someone of the conservative of the conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                    inhibitor of
                                                                                                                                                                                                                                                      cytostatic;
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                      mutant; mutein.
                                                                                                                                                                                                                                                                                    apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23; 1
9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olejniczak ET,
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Q

0,

/note= "N-terminal acetyl"

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RESULT 8
ARBGING ABB7
XX
ABB7
XX
ABB7
XX
ABB7
XX
DT 09-A
XX
DE Fluc
XX
DIAN
KW DIAN
KW human
XX
Homc
OS Synth
XX
FH Key
FT Modil
FT .
PN WO2C
XX
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB76209) acetylated. Claimed smac-derived peptides (see ABB76208-19) bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Modification of the N-terminal alanine destroys all binding affinity for the protein. Thus, Kd values for Bir-3 and Bir-2 were each over 1,000 uM for the present peptide, compared with 0.43 +/ 0.06 uM and 6.0 +/ 0.9 uM, respectively, for the corresponding wild-type peptide. The claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac peptide and an IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI (DIABLO), but with the native N-terminal alanine residue (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide derived from wild-type activator of caspase protein useful f substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                           ABB76228 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a peptide derived from human second mitochondria derived activator of caspase (smac), also known
                                                                                                                                            Synthetic
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis; human; cancer; cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                             Fluorosceinated
                                                                                                                                                                                                                                                                                                  09-AUG-2002
                                                                                                                                                                                                                                                                                                                                        ABB76228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-444169/47
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                                                                                   Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVPIAQKSE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                           smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                              /note= "N-terminal fluorescein"
                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26pp; English
                                                                                                                                                                                                                                                       (DIABLO) derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Betz
                                                                                                                                                                                                                                                                                                                                                                             10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SP,
                                                                                                                                                                                                                                                                                                                                                                             ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human second mitochondria for identifying candidate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
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RESULT 9
ABG72319
ID ABG7
XX ABG7
XX ABG7
XX ABG7
XX Huma
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KW Inhi
KW autc
XX M musc
XX Homc
XX Homc
XX Homc
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XX Homc
XX Homc
XX US2(
XX O2-A
XX O2-A
XX US1-A
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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  WPI; 2003-074681/07
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                       Human; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepatic autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence corresponds to amino acids 1-9 of human second mitochondria derived activator of caspase (smac), also as direct inhibitor of apoptosis binding protein with low pl (DIABLO), but is fluorosceinated. The peptide was used in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activator of caspase protein useful substances to kill cancerous cells
Verhagen AM,
                                        (HALL-)
                                                                                02-MAR-2000;
                                                                                                                        02-MAR-2001; 2001US-0798116
                                                                                                                                                                                                        US2002110851-A1
                                                                                                                                                                                                                                                                                                                                                                                                        Human pro-apoptotic protein DIABLO peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG72319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG72319 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                15-AUG-2002.
                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel peptide derived from wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-444169/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001; 2001WO-US32121
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                                                                                                                                                                                                                                                                                    disease;
                                        HALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVPIAQKSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                        INST MEDICAL RES WALTER & ELIZA.
                                                                                2000AU-0005995
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
  Ekert
                                                                                                                                                                                                                                                                                    immunogen
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100.0%; Pr
  PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Betz
  Vaux DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                               disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is useful for screening for an agent which modulates cell death. An antigen-binding molecule is useful for detecting DIABLO in a biological sample. The agent which modulates the level and/or functional activity of a polypeptide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with expression or activation of DIABLO, such as cancer, vascular disease, hepatic disease, autolumnune disease and neurodegenerative disease, tissue damage or muscular tissue damage associated with heart attack, or hepatic tissue damage associated with a liver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    active fragment of DIABLO (by contacting an inhibitor of apoptosis with a fragment of the polypeptide, and detecting a reduction in act of the IAP), producing a natural or synthetic variant of DIABLO with cell death activity or which reduces IAP activity, an antigenbinding molecule that specifically binds to DIABLO or its fragment, detecting DIABLO in a biological sample (by contacting the sample)
               31-MAR-2000;
23-AUG-2000;
                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                          11-OCT-2001
                                                                                                                                             WO200175067-A2
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                           Novel human diagnostic protein #24789
                                                                                                                                                                                                                                                                                                                     18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                          ABG24798;
                                                                                                                                                                                                                                                                                                                                                                                            ABG24798 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence represents a partial peptide sequence from human DIABLO, identified by protein sequencing of a protein (later identified as DIABLO) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with an IAP and detecting the presence of an IAP/DIABLO complex), modulating the death of a cell (by contacting a cell with an agent, which modulates the level and/or functional activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          death or apoptosis e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               co-precipitates with the human IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 condition comprising an agent which reduces the level/activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression vectors, transformed host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated pro-apoptotic polypeptide, ignated DIABLO, or its biologically active fragment of 8 amino acilength. Also included are the polynucleotide encoding DIABLO, ression vectors, transformed host cells, producing a biologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AVSLVTDST 30
||||||||
1 AVSLVTDST 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Page 4; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
               2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               b; Score 40; DB
b; Pred. No. 21;
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              30
                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein MIHA (not defined).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment of 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IAP)
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RESULT 11
ABB76218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC for identifying expressed genes. (I) is useful in gene therapy techniques (II) or to treat disease states involving (II) (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                         Human smac (DIABLO) derived peptide
                                            WO200230959-A2
                                                                                             Modified-site
                                                                                                                            Misc-difference
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                             DIABLO;
                                                                                                                                                                                                                                                                                                           09-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                               ABB76218;
                                                                                                                                                                                                                                                                                                                                                                              ABB76218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                              human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS88985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colyniclectides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                             smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                             standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPIAQKSEPHSLSSEALMRRAVS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPVHQQMRMHNVAGRATVRQQIS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 55157; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                          inhibitor of apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                          cytostatic; mutant; mutein
                                                                                                                            Location/Qualifiers 5
                                                                           /note=
                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.7%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                           "optional C-terminal
                                                                                                         "wild-type Ala substituted by Phe"
                                                                                                                                                                                                                                                                                                                                                                             9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB
Pred. No. 32;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                          protecting group'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 12
ABB76221
ID ABB76
XX
AC ABB76
XX
DT 09-Al
XX
DE Huma
XX
DE Huma
XX
DE Huma
XX
OS Hom
OS Syni
XX
FT Mis
FT Mis
FT Mo
FT Y
XX
PN WO
XX
PN 18
XX
PF 11
XX
XX
AND
AND
ABB76
ABB76221
ABB76222
ABF76222
ABB76222
ABB76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a peptide derived from wild-type human is second mitochondria derived activator of caspase (smac), also known is second mitochondria derived activator of caspase (smac), also known is second mitochondria derived activator of caspase (smac), also known is second mitochondria derived of compared to the sura and sir derived is peptides (see ABB76208-19) which bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. It is considered to the sura and 2.5 +/- 5.0 in the present peptide, compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively, for the present peptide, compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively, for full-length smac.

Amino acids C-terminal to the isoleucine of smac (DIABLO) are not important for binding to XIAP. The claimed peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the family members.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells - \
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                13-OCT-2000; 2000US-0687549
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human smac (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB76221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB76221 standard; Peptide; 9 AA
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                                                                                  12-OCT-2001; 2001WO-US32121
                                                                                                                                             18-APR-2002
                                                                                                                                                                                                     W0200230959-A2
                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIABLO; smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       smac (DIABLO) peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fesik SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-2000; 2000US-0687549
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                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-444169/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 7; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVPFAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US32121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor of cytostatic;
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                       /note= "optional C-terminal protecting group
                                                                                                                                                                                                                                                                                                               /note= "wild-type Ala substituted by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Betz SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis protein; IAP; apoptosis;
mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olejniczak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prablo), but has the native N-terminal alanine residue (see ABB76209) replaced by glycine. Claimed smac-derived peptides (see ABB76208-19) bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Modification of the N-terminal alanine destroys all binding affinity for the protein. Thus, Kd values for Bir-3 and Bir-2 were each over 1,000 uM for the present peptide, compared with 0.43 +/- 0.06 uM and 6.0 +/- 0.9 uM, respectively, for the corresponding N-terminal Ala peptide. The claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a peptide derived from human seco mitochondria derived activator of caspase (smac), also kn direct inhibitor of apoptosis binding protein with low pI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fesik SW,
                                            13-OCT-2000;
                                                                                                                                                    Modified-site
                                                                                                                                                                                    Key
                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                              human;
                                                                                                                                                                                                                                                         DIABLO;
                                                                                                                                                                                                                                                                                Human smac
                                                                                                                                                                                                                                                                                                       09-AUG-2002
                                                                                                                                                                                                                                                                                                                              ABB76222;
                                                                                                                                                                                                                                                                                                                                                    ABB76222 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 15; 26pp; English
                     (ABBO ) ABBOTT LAB
                                                                  12-OCT-2001; 2001WO-US32121
                                                                                           18-APR-2002
                                                                                                                WO200230959-A2
                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide and an IAP family member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fesik SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conserv
                                                                                                                                                                                                                                            smac; inhibitor of apoptosis protein;
cancer; cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 VPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meadows RP,
Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą,
                                            2000US-0687549
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                           Location/Qualifiers
                                                                                                                                        /note=
                                                                                                                                                             /note= "wild-type Val substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.0%; 50.
100.0%; Pr
                                                                                                                                        "optional C-terminal protecting group"
Betz SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Betz SP,
                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB; Pred. No. 9.3
Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ζ,
2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
9.3e+05;
Olejniczak ET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olejniczak ET,
                                                                                                                                                                                                                                                       IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                               Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            known as
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Sun
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RESULT 14
ABB76225
ID ABB76
XX
ABB7626
AC ABB76
XX
DT 09-AI
XX
DIA
KW DIAB
XX
POS Syn:
XX
FT Mis
FT Moc
FT Moc
FT MO
XX
PD 18
XX
PD 18
XX
PF 12
XX
PF 12
XX
PF 12
XX
PF 12
XX
XX
PF 12
XX
XX
PR 11:
XX
XX
XX
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XX
XX
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Best Local
                             WPI; 2002-444169/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DIABLO), but has the native valine residue (see ABB76209) replaced by alanine. Claimed smac-derived peptides (see ABB76208-19) bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Mutation of the valine of the peptide causes some loss of binding to the protein. Thus, Kd values for Bir-3 and Bir-2 were 12 +/- 2 up and 56 +/- 5 up, respectively, up for the present peptide, compared with 0.43 +/- 0.06 um and 6.0 +/- 0.9 um, respectively, for the corresponding wild-type peptide. The claimed smac-derived peptides can be used to identify candidate with the content of the cont
                                                                           Fesik SW,
                                                                                                                      (ABBO ) ABBOTT LAB
                                                                                                                                                                    13-OCT-2000; 2000US-0687549
                                                                                                                                                                                                                12-OCT-2001; 2001WO-US32121
                                                                                                                                                                                                                                                                18-APR-2002
                                                                                                                                                                                                                                                                                                              W0200230959-A2
                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIABLO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human smac (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB76225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB76225 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a peptide derived from human second mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disrupt the binding interaction between a smac peptide and an IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-444169/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AVPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAPIAQKSE 9
                                                                        Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                   "optional C-terminal protecting group
                                                                                                                                                                                                                                                                                                                                                                                                 "wild-type Ala substituted by Gly"
                                                                      Betz SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide.
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Pred.
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                                                                      Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                      Ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3e+05;
                                                                   Olejniczak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9
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                                                                      ET,
                                                                      Sun
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RESULT 15
ABB76226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                          DIABLO; smac;
                                               WPI; 2002-444169/47.
                                                                          Fesik SW, Meadows RP,
                                                                                                      (ABBO ) ABBOTT LAB
                                                                                                                                 13-OCT-2000; 2000US-0687549
                                                                                                                                                              12-OCT-2001; 2001WO-US32121
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                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                        Human smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB76226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB76226 standard;
                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disrupt the binding interaction between a smac peptide and an family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 15; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVPIAQKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVPIGQKSE
                                                                                                                                                                                                                                                                                                                                                                                                                       (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                             inhibitor of apoptosis protein; IAP; apoptosis;
cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                            /note= "n-propionic acid"
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.0%;
88.9%;
                                                                                                                                                                                                                                               "optional C-terminal protecting group"
                                                                          Betz
                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
                                                                          SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                          Liu
                                                                        z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       و
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,.3e+05;
1;
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                                                                        Olejniczak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                        ET,
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Search completed: October 2, 2003, 09:41:55 Job time : 36 secs
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                                                                                                                                                                                                                                                                                                             The present sequence is a peptide derived from human second control mitochondria derived activator of caspase (smac), also known as condition of direct inhibitor of apoptosis binding protein with low pI (DIABLO), but has the native N-terminal alanine residue (see ABB76209) replaced by propionic acid. Claimed smac-derived peptides (see ABB76209) replaced by propionic acid. Claimed smac-derived peptides (inhibitor of apoptosis protein (IAP) family member. Modification of the N-terminal alanine destroys all binding affinity for the protein. Thus, Kd values for Bir-3 and Bir-2 were each over 1,000 cm M for the present peptide, compared with 0.43 +/- 0.06 uM and 6.0 +/- 0.9 uM, respectively, for the corresponding N-terminal Ala central middles substances which induce or promote apoptosis in cells. The claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac compensation and an IAP family member.
                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 15; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substances to kill cancerous cells
                                                                                        2 VPIAQKSE 9
||||||||
2 VPIAQKSE 9
                                                                                                                                                                                                                                                                            9 AA;
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                    27.0%; Score 38; DB 23; Length 9; 100.0%; Pred. No. 9.3e+05;
                                                                                                                                                                                 0;
                                                                                                                                                                               Mismatches
                                                                                                                                                                                 0; Indels
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